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OM nucleic - nucleic search, using sw model

Run on: August 22, 2004, 13:38:08 ; Search time 508 Seconds
(without alignments)
9447.154 Million cell updates/sec

Title: US-10-024-444B-1
Perfect score: 977

Perfect score: 977
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3228839 seqs, 2456066551 residues

Total number of hits satisfying chosen parameters: 6457678

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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19: /cgn2_6/prodataa1/pubnpa/US60_PUBCOMB.seq: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	977	100.0	977	15	US-10-024-444B-1	Sequence 1, April 1
2	835	85.5	1050	15	US-09-777-789-B	Sequence 8, April 1
3	835	85.5	1351	15	US-10-017-161-309	Sequence 309, April 1
4	835	85.5	1351	16	US-10-029-798-375	Sequence 275, April 1
5	834	85.4	1008	10	US-09-974-591-11	Sequence 11, April 1
6	834	85.4	1008	10	US-09-777-789-10	Sequence 10, April 1
7	834	85.4	1008	10	US-09-974-149-11	Sequence 11, April 1
8	832.4	85.2	1008	10	US-09-974-591-13	Sequence 13, April 1
9	832.4	85.2	1008	10	US-09-974-149-13	Sequence 13, April 1
10	829	84.9	1033	15	US-10-017-161-635	Sequence 635, April 1
11	819.8	83.9	951	9	US-09-886-055-198	Sequence 198, April 1
12	819.8	83.9	951	10	US-09-804-291-198	Sequence 198, April 1
13	819.8	83.9	951	13	US-10-343-650A-513	Sequence 513, April 1
14	819.8	83.9	951	15	US-10-320-362-39	Sequence 39, April 1

15	819.8	83.9	951	16	US-10-300-846-25	Sequence 25, App1
16	414.2	42.4	507	10	US-09-777-889-45	Sequence 45, App1
17	414.2	42.4	528	10	US-09-777-789-40	Sequence 40, App1
18	338	34.6	975	9	US-09-866-055-830	Sequence 430, App1
19	338	34.6	975	10	US-09-804-091-430	Sequence 430, App1
20	338	34.6	975	13	US-10-343-650A-551	Sequence 551, App1
21	338	34.6	975	16	US-10-387-629-139	Sequence 139, App1
22	338	34.6	975	17	US-10-333-946-35	Sequence 35, App1
23	337.6	34.6	951	9	US-09-866-055-482	Sequence 480, App1
24	337.6	34.6	951	10	US-09-804-291-478	Sequence 478, App1
25	337.6	34.6	951	11	US-09-965-422-25	Sequence 25, App1
26	337.6	34.6	984	11	US-09-965-422-29	Sequence 29, App1
27	337.6	34.6	993	11	US-09-965-422-27	Sequence 27, App1
28	337.6	34.6	1351	15	US-10-017-161-7	Sequence 7, App1
29	337.6	34.6	1351	16	US-10-392-198-7	Sequence 7, App1
30	337.6	34.6	1476	17	US-10-473-518-102	Sequence 102, App1
31	336.4	34.4	957	16	US-10-387-629-137	Sequence 137, App1
32	336.4	34.4	1110	9	US-09-866-055-458	Sequence 458, App1
33	336.4	34.4	1110	10	US-09-804-291-458	Sequence 458, App1
34	335	34.3	954	11	US-09-965-422-15	Sequence 15, App1
35	331.8	34.0	954	9	US-09-866-055-482	Sequence 480, App1
36	331.8	34.0	954	10	US-09-804-291-480	Sequence 480, App1
37	331.8	34.0	954	11	US-09-965-422-13	Sequence 13, App1
38	331.8	34.0	1354	15	US-10-017-161-1	Sequence 1, App1
39	331.8	34.0	1354	16	US-10-992-798-1	Sequence 1, App1
40	331.8	34.0	1408	17	US-10-473-518-100	Sequence 100, App1
41	330.2	33.8	958	11	US-09-965-422-31	Sequence 31, App1
42	330.2	33.8	958	11	US-09-965-422-33	Sequence 33, App1
43	330.2	33.8	958	15	US-10-025-806-53	Sequence 53, App1
44	330.2	33.8	958	16	US-10-025-806-53	Sequence 29, App1
45	319.2	32.7	1254	10	US-09-795-271-7	Sequence 7, App1

ALIGNMENTS

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1 RESULT 1
2 US-10-024-444B-1
3 Sequence 1, Application US/1002444B
4 Publication No. US20030165858A1
5 GENERAL INFORMATION:
6 APPLICANT: Padigaru, Muralidhara
7 APPLICANT: Gerlach, Valerie L.
8 APPLICANT: Smithson, Glenna
9 APPLICANT: Stone, David
10 APPLICANT: Bin-Yang, Ruey
11 APPLICANT: Conley, Pamela B.
12 APPLICANT: Hart, Matthew
13 APPLICANT: Tomlinson, James E.
14 APPLICANT: Topper, James N.
15 APPLICANT: Kekuda, Ramesh
16 APPLICANT: Casman, Stacie J.
17 APPLICANT: MacDougall, John R.
18 APPLICANT: Shlomif, Edinger R.
19 TITLE OF INVENTION: No. US20030165858A1el GPCR-like proteins and Nucleic Acids Encodi
20 TITLE OF INVENTION: Same
21 FILE REFERENCE: 21402-224 AG
22 CURRENT APPLICATION NUMBER: US/10/024,444B
23 CURRENT FILING DATE: 2002-12-19
24 PRIOR APPLICATION NUMBER: 60/256635
25 PRIOR FILING DATE: 2000-12-18
26 NUMBER OF SEQ ID NOS: 12
27 SOFTWARE: PatentIn Ver. 2.1
28 SEQ ID NO 1
29 LENGTH: 977
30 TYPE: DNA
31 ORGANISM: Human
32 US-10-024-444B-1

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Query Match	100.0%	Score 977;	DB 15;	length 977;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 977;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 GCACTAAAAACACATCATGAGAGCTCCGGAATCCACCTTGAGAGGGCTTCATCTT 60
 Db 1 GCACTAAAAACACATCATGAGAGCTCCGGAATCCACCTTGAGAGGGCTTCATCTT 60
 QY 61 GGTGGGGAATTCGAATGACAGTGGGCTCTCTGAACTGCTCTATATGATTAACAATCTT 120
 Db 61 GGTGGGGAATTCGAATGACAGTGGGCTCTCTGAACTGCTCTATATGATTAACAATCTT 120
 QY 121 ATTCATGTTGGGCACTGACCGAGCAATGGTCTGCTGCTCTGGCCATCAACCATAGAGCCCG 180
 Db 121 ATTCATGTTGGGCACTGACCGAGCAATGGTCTGCTGCTCTGGCCATCAACCATAGAGCCCG 180
 QY 181 GCTCCACATGCCATGTAATCTCTGCTTGGGAGCTCTCTCATGGAACCTCCGTTTAC 240
 Db 181 GCTCCACATGCCATGTAATCTCTGCTTGGGAGCTCTCTCATGGAACCTCCGTTTAC 240
 QY 241 ATCTGTTGCTACCTCCCAAGGCTTGGGAGCTTCTGCGAGAGAAAACAATACTCTCTT 300
 Db 241 ATCTGTTGCTACCTCCCAAGGCTTGGGAGCTTCTGCGAGAGAAAACAATACTCTCTT 300
 QY 301 TGGAGGCTGTCGACTTCAGATGTTCTGCGACTGACAAATGGGTAGGCTGAGGACCTCT 360
 Db 301 TGGAGGCTGTCGACTTCAGATGTTCTGCGACTGACAAATGGGTAGGCTGAGGACCTCT 360
 QY 361 ACTGAGCTTCATGAGCTATGACAGATATGAGGCAATTTGTCATCTCTGAAATACATGAC 420
 Db 361 ACTGAGCTTCATGAGCTATGACAGATATGAGGCAATTTGTCATCTCTGAAATACATGAC 420
 QY 421 CCTCATAGAGCCCAAGAGCTGCTGAGATCATGAGTGGCCAAATCTCGAATCTCTGATCCCT 480
 Db 421 CCTCATAGAGCCCAAGAGCTGCTGAGATCATGAGTGGCCAAATCTCGAATCTCTGATCCCT 480
 QY 481 GATTGCAATGAGCATATGACAGATATGACATGACATCCCTCTGCTGCTGCTGAGAAAT 540
 Db 481 GATTGCAATGAGCATATGACAGATATGACATGACATCCCTCTGCTGCTGCTGAGAAAT 540
 QY 541 CAGGCACTCTGCTGAGATATGACATGACATGACATGACATGACATGACATGACATGAC 600
 Db 541 CAGGCACTCTGCTGAGATATGACATGACATGACATGACATGACATGACATGACATGAC 600
 QY 601 GATGAGCTTAT 660
 Db 601 GATGAGCTTAT 660
 QY 661 TGTGGCTCTTCAACACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
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 QY 721 GAAAGAAAGCTTGTCACTGCTCTTCCCACTGATTTGTGTGCGGATGTTCTATGAGAC 780
 Db 721 GAAAGAAAGCTTGTCACTGCTCTTCCCACTGATTTGTGTGCGGATGTTCTATGAGAC 780
 QY 781 TGGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 Db 781 TGGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 841 CTCTGTTTTCACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
 Db 841 CTCTGTTTTCACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
 QY 901 TAAAGAGGTCAATGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGG 960
 Db 901 TAAAGAGGTCAATGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGG 960
 QY 961 CAGGCTCTAGGGAAGA 977
 Db 961 CAGGCTCTAGGGAAGA 977

RESULT 2
 US-09-777-789-8
 ; Sequence 8, Application US/09777789
 ; Publication No. US20030087815A1

; GENERAL INFORMATION:
 ; APPLICANT: Padigaru et al.
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 15966-654
 ; CURRENT APPLICATION NUMBER: US/09/777,789
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/180,646
 ; NUMBER OF SEQ ID NOS: 101
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 1050
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-777-789-8

Query Match 85.5%; Score 835; DB 10; Length 1050;
 Best Local Similarity 91.2%; Pred. No. 1,2e-268;
 Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 7 AAAAAACACATCATGAGAGCTCCGGAATCCACCTTGAGAGGGCTTCATCTTGTGGG 66
 Db 59 AAAAAACACATCATGAGAGCTCCGGAATCCACCTTGAGAGGGCTTCATCTTGTGGG 118
 QY 67 GATTCTGATGACAGTGGGCTTCTCTGAACTGCTCTATGCTTACATTTACATCTTATCAT 126
 Db 119 GATTCTGATGACAGTGGGCTTCTCTGAACTGCTCTATGCTTACATTTACATCTTATCAT 178
 QY 127 GTTGGCACTGACAGGAATGGTCTGCTGCTCCGAGCATACCATGAAACCCGGCTCCA 186
 Db 179 GTTGGCCCTGATGACAGGAATGGTCTGCTGCTCCGAGCATACCATGAAACCCGGCTCCA 238
 QY 187 CATGCCATGATACCTCTGCTGCTGGAGCTCTCTCATGAGACCTCTGTTTCAATCTGT 246
 Db 239 CATGCCATGATACCTCTGCTGCTGGAGCTCTCTCATGAGACCTCTGTTTCAATCTGT 298
 QY 247 TGTGATCTCCAAAGCCTTGGCGGACTTCTGCGGAGAGAAAACAATATCTCTTTGGAGG 306
 Db 299 TGTGATCTCCAAAGCCTTGGCGGACTTCTGCGGAGAGAAAACAATATCTCTTTGGAGG 358
 QY 307 CTGTGACCTTCAGATGTTCTGCGACTGACAAATGGGTAGGAGCTCTGATCTGAG 366
 Db 359 CTGTGACCTTCAGATGTTCTGCGACTGACAAATGGGTAGGAGCTCTGATCTGAG 418
 QY 367 CTTCATGAGCTTATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 426
 Db 419 CTTCATGAGCTTATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 478
 QY 427 GAGCCAAAGAGTCTGCTGATCATGATGATGATGATGATGATGATGATGATGATGATG 486
 Db 479 GAGCCAAAGAGTCTGCTGATCATGATGATGATGATGATGATGATGATGATGATGATGATG 538
 QY 487 TATAGCATATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546
 Db 539 TATAGCATATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 598
 QY 547 TGTGCTCTGAGATATCCACCTTGTGAAATGGCTGCTGATGATGATGATGATGATGATG 606
 Db 599 TGTGCTCTGAGATATCCACCTTGTGAAATGGCTGCTGATGATGATGATGATGATGATG 658
 QY 607 GCTTATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 666
 Db 659 GCTTATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 718
 QY 667 CTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726
 Db 719 CTCTATACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 778
 QY 727 AGCCCTTGTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATG 786
 Db 779 AGCCCTTGTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATG 838
 QY 787 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 846

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Db      839 ATTGATGATGCTGTGCTCCAGTTCCTTCACAGACAGCAAGACAATCATCTCTGT 838
QY      847 TTCTACACAAATGTGCTACTCCAGCCCTGAAATCCACTATCAAGCCTGAGAAATAGA 906
Db      899 TTCTACACAAATGTGCTACTCCAGCCCTGAAATCCACTATCAAGCCTGAGAAATAGA 958
QY      907 GGTGATGCGGGCCCTTGAGAGGGGTCTGGGAAAAATACATCTGCTGGACATTCACGCT 966
Db      959 GGTGATGCGGGCCCTTGAGAGGGGTCTGGGAAAAATACATCTGCTGGACATTCACGCT 1018
QY      967 CTAGGGAAGGA 977
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RESULT 3
US-10-017-161-309

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; Sequence 309, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YURAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 309
; LENGTH: 1351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1351)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1151)
US-10-017-161-309

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Query Match 85.5%; Score 835; DB 15; Length 1351;
Best Local Similarity 91.2%; Pred. No. 1.4e-268;
Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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QY      7 AAAAAACACATCATGAGCTCCGAACTCCACCTTGGAGCGGCTTCATCTTGTGGG 66
Db      188 AAGAAACACACATCATGAGCTCCGAACTTCACCTTGGAGAGTGGCTTCATTTTGGTGGG 247
QY      67 GATTCTGAATGACAGTGGGTCTCTGAACTGCTTANGTCACTTACATTCATTCAT 126
Db      248 GATTCTGAATGACAGTGGGTCTCTGAACTGCTTANGTCACTTACATTCATTCATTC 307
QY      127 GTTGGACATGACAGCAATGATGCTGCTGCTGGACCATCACTAGAGCGGCTGCCA 186
Db      308 GTTGGACATGACAGCAATGATGCTGCTGCTGGACCATCACTAGAGCGGCTGCCA 367
QY      187 CATGCCCATGATCTCTGCTTGGGCACTCTCTCATGGAAGCTCTGTTCAATCTGT 246
Db      368 CATGCCCATGATCTCTGCTTGGGCACTCTCTCATGGAAGCTCTGTTCAATCTGT 427
QY      247 TGTCACTCCCAAGGCTTGGCGGACTTTCTGCGGAGAGAAACATATCTCTTGGAGG 306
Db      428 TGTCACTCCCAAGGCTTGGCGGACTTTCTGCGGAGAGAAACATATCTCTTGGAGG 487
QY      307 CTGTGACCTCAAGATGTTCTGCGGACTGACAAATGGATGGCTGAGGACCTCTACTGGC 366
Db      488 CTGTGACCTCAAGATGTTCTGCGGACTGACAAATGGATGGCTGAGGACCTCTACTGGC 547

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QY      367 CTTCATGGCCTATGACAGGTATGTGGCCATTTGTATCTCTTGAATATACATGACCTCAT 426
Db      548 CTTCATGGCCTATGACAGGTATGTGGCCATTTGTATCTCTTGAATATACATGACCTCAT 607
QY      427 GAGCCCAAGATGTGCTGATCATGTGGGCAATCATCTGGATCCTGAGATCCCTGATGGC 486
Db      608 GAGCTCAAGAGCTGTGCTGATCATGTGGGCAATCATCTGGATCCTGAGATCCCTGATGGC 667
QY      487 TATAGACATATCAGATGATACATGACCTCCCTTTCTGTGTCTCTGGAAAAATCAGCA 546
Db      668 CTAATATATATACCGTGTATATCATGACATATCCCTTCTGAGAGGCCCAAGAGATCAGGCA 727
QY      547 TCTGCTCTGTGATATCCACCTTGTGAGAGTTGGCTGTGCTGATATACCTCAGATATGA 606
Db      728 TCTTCTCTGTGATATCCACCTTGTGAGAGTTGGCTGTGCTGATATACCTCAGATATGA 787
QY      607 GCTTATATATATGATGACAGGTGATCTTCTCTGCTCCCATTTCTGCAATGTGGG 666
Db      788 GCTCATGTATATATGATGATGGGTGTGACCTTCTGATTCCTCTTGTGCTGATCTGAC 847
QY      667 CTCTTACACATGATCTTATTCATCTGTGCTTCTGATGCAATGAGGAGAGAA 726
Db      848 CTCTTATACACAAATCTACTGACTGTGTGCTCATATGCCATCAATGAGGAGAGAA 907
QY      727 AGCCCTTGTACCTGCTTCTTCCACCTGATGTGGTGGGATGTCTATGAGACTGGCAC 786
Db      908 AGCCCTTGTACCTGCTTCTTCCACCTGATGTGGTGGGATGTCTATGAGACTGGCAC 967
QY      787 ATTGATGATGCTTGGCCAGTTCTCTTCCACAGCCCAACCAAGACAATCATCTCTGT 846
Db      968 ATTGATGATGCTTGGCCAGTTCTCTTCCACAGCCCAACCAAGACAATCATCTCTGT 1027
QY      847 TTCTACACAAATGTGCTACTCCAGCCCTGAAATCCACTATCAAGCCTGAGAAATAGA 906
Db      1028 TTCTACACAAATGTGCTACTCCAGCCCTGAAATCCACTATCAAGCCTGAGAAATAGA 1087
QY      907 GGTGATGCGGGCCCTTGAGAGGGGTCTGGGAAAAATACATCTGCTGGACATTCACGCT 966
Db      1088 GGTGATGCGGGCCCTTGAGAGGGGTCTGGGAAAAATACATCTGCTGGACATTCACGCT 1147
QY      967 CTAGGGAAGGA 977
Db      1148 CTAGGGAAGGA 1158

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RESULT 4

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US-10-292-798-275
; Sequence 275, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YURAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 275
; LENGTH: 1351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1351)
; FEATURE:

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QY 548 CTGCTCTGTGAGATGCCACCTTGTGTAAGTTGGCTTGTCTGATACCTCCAGGTATGAG 607
 DB 579 CTTCTCTGTGAGATGCCACCTTGTGTAAGTTGGCTTGTCTGATACCTCCAGGTATGAG 638
 QY 608 CTTTAAATATAGTGAGAGAGGTGTGACTTTCCTTGTGCTCCCATTTTGGCATTTGTGGCC 667
 DB 639 CTGATGTATATGTGATGAGAGGTGTGACTTTCCTTGTGCTCCCATTTTGGCATTTGTGGCC 698
 QY 668 TCCACACACTAGTCTTATTCATGCTGTGTGTGATGAGCATGAAATGAGAGAGAGAGAA 727
 DB 699 TCCATATACAAATTTCTACTCATGTGTGTGTGATGAGCATGAAATGAGAGAGAGAGAA 758
 QY 728 GCCCTTGTACCTGTCTTCCCACTGATGTTGTGTGGAGATTTCTATGAGAGCTGCCA 787
 DB 759 GCCCTTGTACCTGTCTTCCCACTGATGTTGTGTGGAGATTTCTATGAGAGCTGCCA 818
 QY 788 TTCAATGATGCTTGGCCAGTTCCCTTCCAGAGCCCAAGAGAGAGAGAGAGAGAGAGAG 847
 DB 819 TTCAATGATGCTTGGCCAGTTCCCTTCCAGAGAGCCCAAGAGAGAGAGAGAGAGAGAG 878
 QY 848 TTCAACAAATTTGATCTCCAGCCCTGATCTCACTCACTCACTCACTCACTCACTCACT 907
 DB 879 TTCAACAAATTTGATCTCCAGCCCTGATCTCACTCACTCACTCACTCACTCACTCACT 938
 QY 908 GTATGCGGGCTTGAAGAGGGTCTTGGAGAAATATACATCTGTGGACATTTCCAGCTC 967
 DB 939 GTATGCGGGCTTGAAGAGGGTCTTGGAGAAATATACATCTGTGGACATTTCCAGCTC 998
 QY 968 TAGGGAAGA 977
 DB 999 TAGGGAAGA 1008

RESULT 6
 US-09-777-789-10
 ; Sequence 10, Application US/09777789
 ; Publication No. US20030087815A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Padigaru et al.
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 15966-654
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/180,646
 ; PRIORITY FILING DATE: 2000-02-07
 ; NUMBER OF SEQ ID NOS: 101
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 1008
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-777-789-10

Query Match 85.4%; Score 834; DB 10; Length 1008;
 Best Local Similarity 91.2%; Pred. No. 2.6e-268;
 Matches 885; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
 QY 8 AAAAAACATCATGAGCTCCGGAACCTTGGAGAGCGGCTTCATCTGGAGG 67
 DB 39 AACTACACAGCATGAGCTCTGGAACCTTGGAGAGCGGCTTCATCTGGAGG 98
 QY 68 ATTCTGAATGACAGTGGGTCTCTGAACTGCTATGCTCAATTTACATCTCATAG 127
 DB 99 ATTCTGAATGACAGTGGGTCTCTGAACTGCTATGCTCAATTTACATCTCATAG 158
 QY 128 TTGGCACTGACCGAGATGTGTCTGTCTCTGCACTACCATAGAGAGCGGCTCCAC 187
 DB 159 TTGGCCCTGATGAGCAATGGCTCTACTGCTCTGCTATACACAGAGAGCGGCTCCAC 218
 QY 188 ATGCCCATGATACCTCTGCTTGGAGAGCTCTCTCTCATGAGAGCGGCTTCATCTGT 247
 DB 219 ATGCCCATGATACCTCTGCTTGGAGAGCTCTCTCTCATGAGAGCGGCTTCATCTGT 278

QY 248 GTCACTCCCAAGGCGCTTGGGAGACTTCTGTGAGAGAGAGAGAGAGAGAGAGAG 307
 DB 279 GTCACTCCCAAGGCGCTTGGGAGACTTCTGTGAGAGAGAGAGAGAGAGAGAGAG 338
 QY 308 TGTGCACTTCAAGATGTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
 DB 339 TGTGCACTTCAAGATGTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 398
 QY 368 TTCAATGATGCTTGGCCAGTTCCCTTCCAGAGCCCAAGAGAGAGAGAGAGAGAG 427
 DB 399 TTCAATGATGCTTGGCCAGTTCCCTTCCAGAGCCCAAGAGAGAGAGAGAGAGAG 458
 QY 428 AGCCCAAGAGCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
 DB 459 AGCCCAAGAGCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 518
 QY 488 ATGAGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 547
 DB 519 ATGAGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578
 QY 548 CTGCTCTGTGAGATGCCACCTTGTGTAAGTTGGCTTGTCTGATACCTCCAGGTATGAG 607
 DB 579 CTTCTCTGTGAGATGCCACCTTGTGTAAGTTGGCTTGTCTGATACCTCCAGGTATGAG 638
 QY 608 CTTTAAATATAGTGAGAGAGGTGTGACTTTCCTTGTGCTCCCATTTTGGCATTTGTGGCC 667
 DB 639 CTGATGTATATGTGATGAGAGGTGTGACTTTCCTTGTGCTCCCATTTTGGCATTTGTGGCC 698
 QY 668 TCCACACACTAGTCTTATTCATGCTGTGTGTGATGAGCATGAAATGAGAGAGAGAGAA 727
 DB 699 TCCATATACAAATTTCTACTCATGTGTGTGTGATGAGCATGAAATGAGAGAGAGAGAA 758
 QY 728 GCCCTTGTACCTGTCTTCCCACTGATGTTGTGTGGAGATTTCTATGAGAGCTGCCA 787
 DB 759 GCCCTTGTACCTGTCTTCCCACTGATGTTGTGTGGAGATTTCTATGAGAGCTGCCA 818
 QY 788 TTCAATGATGCTTGGCCAGTTCCCTTCCAGAGCCCAAGAGAGAGAGAGAGAGAGAG 847
 DB 819 TTCAATGATGCTTGGCCAGTTCCCTTCCAGAGAGCCCAAGAGAGAGAGAGAGAGAGAG 878
 QY 848 TTCAACAAATTTGATCTCCAGCCCTGATCTCACTCACTCACTCACTCACTCACTCACT 907
 DB 879 TTCAACAAATTTGATCTCCAGCCCTGATCTCACTCACTCACTCACTCACTCACTCACT 938
 QY 908 GTATGCGGGCTTGAAGAGGGTCTTGGAGAAATATACATCTGTGGACATTTCCAGCTC 967
 DB 939 GTATGCGGGCTTGAAGAGGGTCTTGGAGAAATATACATCTGTGGACATTTCCAGCTC 998
 QY 968 TAGGGAAGA 977
 DB 999 TAGGGAAGA 1008

RESULT 7
 US-09-974-149-11
 ; Sequence 11, Application US/0974149
 ; Publication No. US2003017505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aliebrook II, John P.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Grose, William M.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Bader, Joel S.
 ; TITLE OF INVENTION: Methods of Use for No. US2003017505A1 Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
 ; FILE REFERENCE: 15966-654UB
 ; CURRENT FILING DATE: 2002-05-20

PRIOR APPLICATION NUMBER: 60/323,755
 PRIOR FILING DATE: 2001-09-20
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 11
 LENGTH: 1008
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (27)..(998)
 US-09-974-149-11

Query Match 85.4%; Score 834; DB 10; Length 1008;
 Best Local Similarity 91.2%; Pred. No. 2,66-268;

Matches 885; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

8 AAAAAACATCATCAGAGCTCCGAACTCCACCTTGGGAGCGCTTCATCTTGGTGGG 67
 39 AACTACACAGCATGAGCTCGAATCTTCACTTGGGAGTGGCTTCACTTGGTGGG 98
 68 ATTCTGAATGACAGTGGCTCTCTGAATCTCTATGCTATGCTATTAACAATCTTACATG 127
 99 ATTCTGAATGACAGTGGCTCTCTGAATCTCTATGCTATGCTATTAACAATCTTACATG 158
 128 TTGGACACGACGAGCAATGGTCTGGCTCCGACATCAGCATGAGAGCCGCTCCAC 187
 159 TTGGCCCTGATGACGAGTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 218
 188 ATGCCCATGATACCTCTGCTGGGAGCTCTCTCATGATGACCTCTGTTCACTGTT 247
 219 ATGCCCATGATACCTCTGCTGGGAGCTCTCTCATGATGACCTCTGTTCACTGTT 278
 248 GTCACTCCCAAGGCTTGGCGGACTTTCTGGCGAGAGAAACATATCTCTTGGAGGC 307
 279 GTCACTCCCAAGGCTTGGCGGACTTTCTGGCGAGAGAAACATATCTCTTGGAGGC 338
 308 TGTGACCTTGCATGATGCTCTGGGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
 339 TGTGACCTTGCATGATGCTCTGGGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 398
 368 TTCAATGAGCTATGACAGATGATGGGAGCTTGTCACTCTGTAATACATGACCTCTCATG 427
 399 TTCAATGAGCTATGACAGATGATGGGAGCTTGTCACTCTGTAATACATGACCTCTCATG 458
 428 AGCCCAAGAGTGTCTGATGATGATGGGAGCTTGTCACTCTGTAATACATGACCTCTCATG 487
 459 AGCTCAAGAGCTGTCTGATGATGATGGGAGCTTGTCACTCTGTAATACATGACCTCTCATG 518
 488 ATAGGACATGACATGATGATGATGGGAGCTTGTCACTCTGTAATACATGACCTCTCATG 547
 519 CTAATATATACAGTATGATGATGGGAGCTTGTCACTCTGTAATACATGACCTCTCATG 578
 548 CTGCTGTGAGATGCCACCTTGTGTAATGAGCTGTGTAATGAGCTGTGTAATGAGCTGTGTA 607
 579 CTCTCTGTGAGATGCCACCTTGTGTAATGAGCTGTGTAATGAGCTGTGTAATGAGCTGTGTA 638
 608 CTCTCTGTGAGATGCCACCTTGTGTAATGAGCTGTGTAATGAGCTGTGTAATGAGCTGTGTA 667
 639 CTCTCTGTGAGATGCCACCTTGTGTAATGAGCTGTGTAATGAGCTGTGTAATGAGCTGTGTA 698
 668 TCCCTACACATGATGATGATGATGGGAGCTTGTCACTCTGTAATACATGAGAGAGAGAGAG 727
 699 TCCCTACACATGATGATGATGATGGGAGCTTGTCACTCTGTAATACATGAGAGAGAGAGAG 758
 728 GGCCTTGTGATGATGATGATGATGGGAGCTTGTCACTCTGTAATACATGAGAGAGAGAGAG 787
 759 GGCCTTGTGATGATGATGATGATGGGAGCTTGTCACTCTGTAATACATGAGAGAGAGAGAG 818
 788 TTCAATGATGATGATGATGATGGGAGCTTGTCACTCTGTAATACATGAGAGAGAGAGAGAG 847
 819 TTCAATGATGATGATGATGATGGGAGCTTGTCACTCTGTAATACATGAGAGAGAGAGAGAG 878

848 TTCTACAAATTTGATCAGCTCCAGCTTGAATCAGCTATCATCAGCTGAGAGATAAGAG 907
 879 TTCTACAAATTTGATCAGCTCCAGCTTGAATCAGCTATCATCAGCTGAGAGATAAGAG 938
 908 GTCAATGAGAGCTTGAAGAGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
 939 GTCAATGAGAGCTTGAAGAGAGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 998
 968 TAGGAGAGAG 977
 999 TAGGAGAGAG 1008

RESULT 8

US-09-974-591-13
 Sequence 13, Application US/09974591
 Publication No. US20030059830A1

GENERAL INFORMATION:

APPLICANT: Alsobrook II, John P

APPLICANT: Burgess, Catherine E

APPLICANT: Grose, William M

APPLICANT: Lepley, Denise M

APPLICANT: Padigaru, Muralidhara

APPLICANT: Spylek, Kimberly A

TITLE OF INVENTION: No. US20030059830A1 Single Nucleotide Polymorphisms for Olfactory

TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding

FILE REFERENCE: 15966-654 CIP

CURRENT APPLICATION NUMBER: US/09/974,591

CURRENT FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/245,292

PRIOR FILING DATE: 2000-11-02

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 1008

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (27)..(998)

US-09-974-591-13

Query Match 85.2%; Score 832.4; DB 10; Length 1008;
 Best Local Similarity 91.1%; Pred. No. 8,86-268;

Matches 884; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

8 AAAAAACATCATCAGAGCTCCGAACTCCACCTTGGGAGCGGCTTCACTTGGTGGG 67
 39 AACTACACAGCATGAGCTCGAATCTTCACTTGGGAGTGGCTTCACTTGGTGGG 98
 68 ATTCTGAATGACAGTGGCTCTCTGAATCTCTATGCTATGCTATTAACAATCTTACATG 127
 99 ATTCTGAATGACAGTGGCTCTCTGAATCTCTATGCTATGCTATTAACAATCTTACATG 158
 128 TTGGACACGACGAGCAATGGTCTGGCTCCGACATCAGCATGAGAGCCGCTCCAC 187
 159 TTGGCCCTGATGACGAGTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 218
 188 ATGCCCATGATACCTCTGCTGGGAGCTTGTCTGATGAGAGCTCTGTTCACTGTT 247
 219 ATGCCCATGATACCTCTGCTGGGAGCTTGTCTGATGAGAGCTCTGTTCACTGTT 278
 248 GTCACTCCCAAGGCTTGGCGGAGCTTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307
 279 GTCACTCCCAAGGCTTGGCGGAGCTTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 338
 308 TGTGACCTTGCATGATGCTCTGGGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
 339 TGTGACCTTGCATGATGCTCTGGGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 398
 368 TTCAATGAGCTATGACAGTATGATGGGAGCTTGTCACTCTGTAATACATGAGAGAGAGAGAG 427

Db 399 TTCAATGCGCTATGACAGGATATGAGGCAATTTGTATCTCTGACATACATGACCTCATG 458
Qy 428 AGCCCAAGATGCTGCTGATCATATGAGTGGCCACATCTGGATCTGGACATCCCTGATTTGCT 487
Db 459 AGCTCAAGAGCTGCTGCTGATCATATGAGTGGCCACATCTGGATCTGGACATCCCTGATTTGCT 518
Qy 488 ATAGACATACATGATATGACATATGACATCTCTCTCTGATGCTGCTGAGAAATCAGGAT 547
Db 519 CTATATATATACCGGTATATACATGACATATCTCTCTGACAGGCGCCAGAGATCAGGAT 578
Qy 548 CTGCTCTGATGATCCCAACCTTGGCTGAAATGGCTGCTGATGATCTGACAGGATGAG 607
Db 579 CTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638
Qy 608 CTATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
Db 639 CTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
Qy 668 TCCATACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
Db 699 TCCATATACAAATTTCTATCTACTGATGCTCATATGCTCATMAATGAGGAGAGAGAGAA 758
Qy 728 GCCCTTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 787
Db 759 GCCCTTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 818
Qy 788 TTCAATGATGCTTCTCCCAATTTCTCTTCCACAGCCCAACAGCAACATCATCTCTGTT 847
Db 819 TTCAATGATGCTTCTCCCAATTTCTCTTCCACAGCAACAGCAACATCATCTCTGTT 878
Qy 848 TTCAACAAATTTGATCTCCAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
Db 879 TTCAACAAATTTGATCTCCAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
Qy 908 GTCAATGCGGCGCTTGAAGAGGAGGCTCTGGAGAAATATACATGCTGAGCATTTCCACGCTC 967
Db 939 GTCAATGCGGCGCTTGAAGAGGAGGCTCTGGAGAAATATACATGCTGAGCATTTCCACGCTC 998
Qy 968 TAGGAAAGGA 977
Db 999 TAGGAAAGGA 1008

RESULT 9
US-09-974-149-13
; Sequence 13, Application US/09974149
; Publication No. US20030175705A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Groese, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Bader, Joel S
; APPLICANT: Batsal, Aruna
; TITLE OF INVENTION: Methods of Use for No. US20030175705A1 Single Nucleotide
; TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
; FILE REFERENCE: 15966-654UB
; CURRENT APPLICATION NUMBER: US/09/974,149
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/323,755
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(998)

US-09-974-149-13
Query Match 85.2%; Score 832.4; DB 10; Length 1008;
Best Local Similarity 91.1%; Pred. No. 8,88-268;
Matches 884; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 8 AAAAAACATCATGATGAGCTCCGGAATCTCAACCTTGGAGACGGCTTATCTTGGTGGG 67
Db 39 AACTATACACAGCATGAGAGCTCTGGAACCTTCACTTGGAGAGTGGCTTATTTGGTGGG 98
Qy 68 ATTGTAATGACATGAGGCTCCCGAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 127
Db 99 ATTGTAATGACATGAGGCTCCCGAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 158
Qy 128 TTGGCACTGACCAACAAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Db 159 TTGGCACTGACCAACAAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 218
Qy 188 ATGCCATGTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
Db 219 ATGCCATGTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 278
Qy 248 GTCACTCCCAAGGCTTGGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
Db 279 GTCACTCCCAAGGCTTGGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 338
Qy 308 TGTCACCTTACATGATGCTTGGCACTGACATGAGGATAGCTGAGGACCTTCTACTGAGCC 367
Db 339 TGTCACCTTACATGATGCTTGGCACTGACATGAGGATAGCTGAGGACCTTCTACTGAGCC 398
Qy 368 TTCAATGCTTATGACAGGATATGAGGATTTGTATCTCTGTAATATATATACCTCTATG 427
Db 399 TTCAATGCTTATGACAGGATATGAGGATTTGTATCTCTGTAATATATATACCTCTATG 458
Qy 428 AGCCCAAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
Db 459 AGCTCAAGAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 518
Qy 488 ATAGACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 547
Db 519 CTATATATATACCGGTATATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578
Qy 548 CTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 607
Db 579 CTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638
Qy 608 CTATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
Db 639 CTATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
Qy 668 TCCATACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
Db 699 TCCATATACAAATTTCTATCTACTGATGCTCATATGCTCATMAATGAGGAGAGAGAGAA 758
Qy 728 GCCCTTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 787
Db 759 GCCCTTGACCTGCTCTTCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 818
Qy 788 TTCAATGATGCTTCTCCCAATTTCTCTTCCACAGCCCAACAGCAACATCATCTCTGTT 847
Db 819 TTCAATGATGCTTCTCCCAATTTCTCTTCCACAGCAACAGCAACATCATCTCTGTT 878
Qy 848 TTCAACAAATTTGATCTCCAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
Db 879 TTCAACAAATTTGATCTCCAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
Qy 908 GTCAATGCGGCGCTTGAAGAGGAGGCTCTGGAGAAATATACATGCTGAGCATTTCCACGCTC 967
Db 939 GTCAATGCGGCGCTTGAAGAGGAGGCTCTGGAGAAATATACATGCTGAGCATTTCCACGCTC 998
Qy 968 TAGGAAAGGA 977
Db 999 TAGGAAAGGA 1008

RESULT 13
 US-10-343-650A-513
 ; Sequence 513, Application US/10343650A
 ; Publication No. US20040067499A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HAGA, TATSUYA
 ; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: 31671-186347
 ; CURRENT APPLICATION NUMBER: US/10/343,650A
 ; CURRENT FILING DATE: 2003-07-21
 ; PRIOR APPLICATION NUMBER: JP 2000/237818
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: JP 2001/34434
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 694
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 513
 ; LENGTH: 951
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(951)
 US-10-343-650A-513

Query Match 83.9%; Score 819.8; DB 13; Length 951;
 Best Local Similarity 91.4%; Pred. No. 1.4e-263;
 Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

20 ATGAGAGCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 79
 1 ATGAGAGCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 60
 80 AGTGGGTCTCTGAACTGCTCTATGCTACATTTACATTCCTATACATGTTGGACCTGACC 139
 61 AGTGGGTCTCTGAACTGCTCTATGCTACATTTACATTCCTATACATGTTGGACCTGACC 120
 140 AGCAATGCTGCTGCTGCTCCGAGCATCAACATAGAGCGGCTCCACATGCCCATGTAC 199
 121 AGCAATGCTGCTGCTGCTCCGAGCATCAACATAGAGCGGCTCCACATGCCCATGTAC 180
 200 CTCCTGCTGGGAGAGCTCTCTCTCATAGACCTCTCTGACATCTGTTGACCTCCCAAG 259
 181 CTCCTGCTGGGAGAGCTCTCTCTCATAGACCTCTCTGACATCTGTTGACCTCCCAAG 240
 260 GCTTTGGGAGAGCTTTCTGCGGAGAGAAACACTATCTCTTGGAGGCTGGACCTTCAG 319
 241 GCTTTGGGAGAGCTTTCTGCGGAGAGAAACACTATCTCTTGGAGGCTGGACCTTCAG 300
 320 ATGTTCTCGGAGAGCTGAGAAATGGGTAGAGGCTGAGAGCTCTACTAGGCTTCATGGCCTAT 379
 301 ATGTTCTCGGAGAGCTGAGAAATGGGTAGAGGCTGAGAGCTCTACTAGGCTTCATGGCCTAT 360
 380 GACAGGATATGAGCATTGTCTATCTCTGAAATACATGACCTCTATGAGCCCAAGAGTC 439
 361 GACAGGATATGAGCATTGTCTATCTCTGAAATACATGACCTCTATGAGCCCAAGAGTC 420
 440 TGTGATGATGAGTGGGAGAGCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAG 499
 421 TGTGATGATGAGTGGGAGAGCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAG 480
 500 ATGATGATGATGAGCCTGCTCTCTGATGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAG 559
 481 ATGATGATGATGAGCCTGCTCTCTGATGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAG 540
 560 ATCCACAGCTTGTGAGTGGCTGTGATGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAG 619
 541 ATCCACAGCTTGTGAGTGGCTGTGATGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAG 600
 620 GTGACAGGTGAGATCTTCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 679
 601 GTGATGAGGTGAGATCTTCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 660

*

Query 680 GTTCTATTCAGTGTGCTTGTGATGCTCATTAATGAGGGAGAGAAAGCCCTTGTACCC 739
 661 ATTCTACTACTGTGTCTCATATGACCATCAATGAGGGAGAGAAAGCCCTTGTACCC 720
 740 TGTCTTCTCCAGCTGATTTGTGTGCGGAGATGTTCTATGAGCTGCGCATTCATGATGTC 799
 721 TGTCTTCTCCAGCTGATTTGTGTGCGGAGATGTTCTATGAGCTGCGCATTCATGATGTC 780
 800 TTGCCAGTTCCTTCCAGAGCCCAAG 859
 781 TTGCCAGTTCCTTCCAG 840
 860 GTCACTTCAGCCCTGATATCATCTATCTAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 919
 841 GTCACTTCAGCCCTGATATCATCTATCTAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 920 TTGAGAGAGGTCTCTGAGAAATATCATATGCTGAGCATTCAGAGCTCTAG 970
 901 TTGAGAGAGGTCTCTGAGAAATATCATATGCTGAGCATTCAGAGCTCTAG 951

RESULT 14

US-10-220-382-39
 ; Sequence 39, Application US/10220382
 ; Publication No. US2003011911A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: LAL, Preeti
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: PATTERSON, Chandra
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: SHIH, Leo L.
 ; APPLICANT: TRIBOULEY, Catherine
 ; APPLICANT: LU, Dying Aina M.
 ; APPLICANT: YUE, Henry
 ; APPLICANT: KHAN, Farrah A.
 ; APPLICANT: POLICKI, Jennifer L.
 ; APPLICANT: AD-YOUNG, Janice
 ; APPLICANT: YANG, Junming
 ; APPLICANT: HARLAND, Lee
 ; APPLICANT: WALSH, Roderick T.
 ; APPLICANT: LO, Terence P.
 ; APPLICANT: BOROMSKY, Mark L.
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: PI-0044 PCT
 ; CURRENT APPLICATION NUMBER: US/10/220,382
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
 ; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 39
 ; LENGTH: 951
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US2003011911A1 7472446CHI
 US-10-220-382-39

Query Match 83.9%; Score 819.8; DB 15; Length 951;
 Best Local Similarity 91.4%; Pred. No. 1.4e-263;
 Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

20 ATGAGAGCTCCGGAAGCTCAGCTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 79
 1 ATGAGAGCTCCGGAAGCTTCACTTGGAGAGCGGCTTCACTTGGTGGGAGTTCTGAATGAC 60
 80 AGTGGGTCTCTGAACTGCTCTATGCTACATTTACATTCCTATACATGTTGGACATGACC 139
 61 AGTGGGTCTCTGAACTGCTCTATGCTACATTTACATTCCTATACATGTTGGACATGACC 120
 140 AGCAATGCTGCTGCTGCTCCGAGCATCAACATAGAGCGGCTCCACATGCCCATGTAC 199

Db 121 AGCAATGGCTACTGCTCTGCTGCTATACCAATGGAAGCCGGCTCCACATGCCATGAC 180
QY 200 CTCCTGCTGGGGAGCTCTCTCTATATGAACTCTCTGTTACATCTGTTGCACTCCCAAG 259
Db 181 CTCCTGCTGGGGAGCTCTCTCTATATGAACTCTCTGTTACATCTGTTGCACTCCCAAG 240
QY 260 GCTTGGGGAGCTCTCTCTGCGAGAGAAACATATCTCTCTTGGAGGCTGGCACTTAC 319
Db 241 GCCCTTGGGGAGCTCTCTCTGCGAGAGAAACATATCTCTCTTGGAGGCTGGCACTTAC 300
QY 320 ATGTTCTGCACTGACAAATGAGTAGGCTGAGGAGCTCTCTCTCTCTCTCTCTCTCT 379
Db 301 ATGTTCTGCACTGACAAATGAGTAGGCTGAGGAGCTCTCTCTCTCTCTCTCTCTCT 360
QY 380 GACAGGATGAGGAGCT 439
Db 361 GACAGGATGAGGAGCT 420
QY 440 TGCTGATCAATGAGGAGCAATCTGATCTGAGGAGCTCTCTCTCTCTCTCTCTCTCT 499
Db 421 TGCTGATCAATGAGGAGCAATCTGATCTGAGGAGCTCTCTCTCTCTCTCTCTCTCT 480
QY 500 ATGTACATATGACCT 559
Db 481 GTGTATACATATGACCT 540
QY 560 ATCCCACTCTGCTGAAAGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Db 541 ATCCCACTCTGCTGAAAGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
QY 620 GTGACAGGAGTGAATCT 679
Db 601 GTGATGAGGAGTGAATCT 660
QY 680 GTGCTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 739
Db 661 ATCTTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 740 TGCT 799
Db 721 TGCT 780
QY 800 TTGCCCAGTCT 859
Db 781 TTGCCCAGTCT 840
QY 860 GTCACTCCAGCCCTGATCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 919
Db 841 GTCACTCCAGCCCTGATCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
QY 920 TTGAGGAGGCT 970
Db 901 TTGAGGAGGCT 951

RESULT 15
US-10-300-846-25
; Sequence 25, Application US/10300846
; Publication No. US20030207337A1
; GENERAL INFORMATION:
; APPLICANT: HAN, YI
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ECHEVERRI, FERNANDO
; APPLICANT: WANG, KUN
; TITLE OF INVENTION: OLFACTORY RECEPTORS FOR ISOVALERIC ACID AND RELATED
; TITLE OF INVENTION: MALODORANTS AND USE THEREOF IN ASSAYS FOR
; FILE REFERENCE: 078003-0291924
; CURRENT APPLICATION NUMBER: US/10/300,846
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/348,371
; PRIOR FILING DATE: 2002-01-16

QY PRIOR APPLICATION NUMBER: 09/809,291
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/341,872
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-300-846-25

Query Match 83.9%; Score 819.8; DB 16; Length 951;
Best Local Similarity 91.4%; Pred. No. 1.4e-263;
Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 20 ATGAGGCTCCGGAATCCACTTGGGAGGCGCTTCACTTGGGGATTTGGAATGAC 79
Db 1 ATGAGGCTCCGGAATCCACTTGGGAGGCGCTTCACTTGGGGATTTGGAATGAC 60
QY 80 AGTGGGCTCTGAACTGCTCTATGCTACATTTAACAATCTATACATGTTGGACATGAC 139
Db 61 AGTGGGCTCTGAACTGCTCTATGCTACATTTAACAATCTATACATGTTGGACATGAC 120
QY 140 AGCAATGCTGCTGCT 139
Db 121 AGCAATGCTGCTGCT 180
QY 200 CTCCTGCTGGGGAGCT 259
Db 181 CTCCTGCTGGGGAGCT 240
QY 260 GCTTGGGGAGCTCTCTCTGCGAGAGAAACATATCTCTCTTGGAGGCTGGCACTTAC 319
Db 241 GCCCTTGGGGAGCTCTCTCTGCGAGAGAAACATATCTCTCTTGGAGGCTGGCACTTAC 300
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Search completed: August 22, 2004, 15:42:45
Job time : 511 secs

OM nucleic - nucleic search, using sw model

Run on: August 22, 2004, 12:56:50 ; Search time 3874 Seconds

(without alignments)
10930.858 Million cell updates/sec

Title: US-10-024-444B-1
Perfect score: 977

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Scoring table: IDENTITY_NUC

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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No.	Score	Match	length	DB	ID
					Description

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C	3	965	98.8	1350	9	AB065539	Hom sapi
C	4	965	98.8	208430	2	AC027641	Hom sapi
C	5	936	95.8	947	6	AX241682	Sequence
C	6	835	85.5	1050	6	AX102048	Sequence
C	7	835	85.5	1351	6	AX466083	Sequence
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C	10	835	85.5	173611	9	AC087280	Hom sapi
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AX686711			PAT 29-MAR-2003

DEFINITION Sequence 1 from Patent WO02070707.

VERSION AX686711.1 GI:29372291

SOURCE Homo sapiens (human)

ORGANISM

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

TITLE Gpcr-like proteins and nucleic acids encoding same
JOURNAL Patent: WO 02070707-A 1 12-SEP-2002;
Corporation (US); COR THERAPEUTICS, INC. (US)
FEATURES Location/Qualifiers
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RESULT 2
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LOCUS Homo sapiens chromosome 11, clone RP11-732A19, complete sequence.
DEFINITION AC091564
AC091564.12 GI:22657585
VERSION
KEYWORDS
HNG.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 211735)
Birren, B., Nussbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-732A19
Unpublished
2 (bases 1 to 211735)
Birren, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Boguslavsky, L., Bouhagalter, B., Brown, A.,
Camata, J., Campiano, A., Chang, D., Choepel, Y., Colangelo, M.,
Collins, S., Collamore, A., Cooke, P., DeRellano, K., Dewar, K.,
Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D.,
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Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,
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Maclean, C., Macdonald, P., Margulis, N., Matthews, C., McCarthy, M.,
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Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., North, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, D.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
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Scolanovic, N., Strauss, N., Subramanian, A., Talamas, J., Teste, S.,
Theodore, J., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 211735)
REFERENCE
AUTHORS
Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhagalter, B.,
Camata, J., Chang, J., Chazaro, B., Choepel, Y., Collamore, A.,
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Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
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O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
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Zembek, L., Zimmer, A. and Zody, M.
TITLE
JOURNAL
Submitted (13-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE
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SOURCE Homo sapiens
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Waterston, R.H.
JOURNAL The sequence of Homo sapiens clone
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 208430)
JOURNAL Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 17, 2000 this sequence version replaced gi:7344780.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WTGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H NH0732A19
----- Summary Statistics -----

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Sequencing vector: plasmid; 2%
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Assembly program: Phrap; version 0.990319
Consensus quality: 198825 bases at least Q40
Consensus quality: 202103 bases at least Q30
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Insert size: 219000; agarose-fp
Quality coverage: 4.27 in Q20 bases; agarose-fp
Quality coverage: 4.55 in Q20 bases; sum-of-coverage
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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ORIGIN

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Query Match      98.8%; Score 965; DB 2; Length 208430;
Best Local Similarity 99.9%; Pred. No. 9.3e-276;
Matches 976; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 GCACCTAAAAAACATCATGAGCTCCGGAACCTTCGGAAGCGGCTTCACTT 60
DB      52629 GCAACTAAAAAACACATCATGAGCTCCGGAACCTTCGGAAGCGGCTTCACTT 52570
QY      61 GGTGGGATTTGATGACAGTGGGTCTCTGAACTGCTTATGTAATTTAACTCT 120
DB      52569 GGTGGGATTTGATGACAGTGGGTCTCTGAACTGCTTATGTAATTTAACTCT 52510
QY      121 ATATCATTTGGGCACTATACAGAAATGTCGTCCTCGGCATCACCATGAAACCGG 180
DB      52509 ATATCATTTGGGCACTATACAGAAATGTCGTCCTCGGCATCACCATGAAACCGG 52450
QY      181 GCTCCACATGCCCATGATCTCTGCTGGGAGCTCTCTCATGAGACCTCTGTTCA 240
DB      52449 GCTCCACATGCCCATGATCTCTGCTGGGAGCTCTCTCATGAGACCTCTGTTCA 52390
QY      241 ATCTGTTGCTACCTCCCAAGGCTTGGGGACTTTCTGCGAGAGAAAAACATATCTCT 300
DB      52389 ATCTGTTGCTACCTCCCAAGGCTTGGGGACTTTCTGCGAGAGAAAAACATATCTCT 52331
QY      301 TGAAGGCTGGGCACTTCAAGATGTTCTCGGCACTGACAAATGGTAGGCTGAGACCTCT 360
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QY      361 ACTGGCCTTATGAGCTATGACAGATATGAGGCAATTTGTCATCTCTGAAATATCATGAC 420
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QY      421 CCTATAGAGCCCAAGAGTCTGCTGATCATATGAGGCAATCTCTGATCTCTGAGATCTCT 480
DB      52210 CCTATAGAGCCCAAGAGTCTGCTGATCATATGAGGCAATCTCTGATCTCTGAGATCTCT 52151
QY      481 GATTGCTATGACATACATGATGACATATGACATCTCCCTTCTGATGCTCTGAGAAAT 540
DB      52150 GATTGCTATGACATACATGATGACATATGACATCTCCCTTCTGATGCTCTGAGAAAT 52091
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DB      51970 TGTGGCTCTCTACACACTAGTCTTATTCATCTGCTGCTGTATGTCATCAATGAGGGAG 51911
QY      721 GAAGAAAGCCCTTTCACCTGCTCTTCCACCTGATGTTGCTCGGAGATTTCTATGAGAC 780
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QY      781 TGCCACATTCATGATATGTTCTTGCCAGTTCTCTTCACAGCCCAACAAACAATATAT 840
DB      51850 TGCCACATTCATGATATGTTCTTGCCAGTTCTCTTCACAGCCCAACAAACAATATAT 51791
QY      841 CTCTGTTTCTTACACATTTGTCATCTCCAGCCCTGAATTCATCTACAGCTGAGGAA 900
DB      51790 CTCTGTTTCTTACACATTTGTCATCTCCAGCCCTGAATTCATCTACAGCTGAGGAA 51731
QY      901 TAAGGAGGTCAAGCGGCTTGAGAGGGTCTCTGGAATAATACATATCTGTGGCAATTC 960
DB      51730 TAAGGAGGTCAAGCGGCTTGAGAGGGTCTCTGGAATAATACATATCTGTGGCAATTC 51671
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RESULT 5
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LOCUS      AX241682          947 bp      DNA      linear      PAT 26-SEP-2001
DEFINITION Sequence 430 from Patent WO0127158.
ACCESSION  AX241682
VERSION     AX241682.1 GI:15798557
KEYWORDS   .
SOURCE      synthetic construct
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            artificial sequences.
REFERENCE   1 Bellenson, J., Smith, D., Lancet, D., Glusman, G., Fuchs, T. and
            Yanai, I.
            Olfactory receptor sequences
            Patent: WO 0127158-A 430 19-Apr-2001;
            Disclants (US) ; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
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ORIGIN
Query Match      95.8%; Score 936; DB 6; Length 947;
Best Local Similarity 99.9%; Pred. No. 2.1e-267;
Matches 947; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY      80 AGTGGGCTCTCTGAACCTGCTCTATGCTACATTTTAACTTCTATACATGTTGGCACTGACC 139
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QY      140 AGCAATGCTGCTGCTCTCTGCGCATACATAGAAACCGGCTCCGACATGCCCATGTAC 199
DB      121 AGCAATGCTGCTGCTCTCTGCGCATACATAGAAACCGGCTCCGACATGCCCATGTAC 180
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Db 181 CTCCTGCTGGGAGGCTCTCTCATGAGACCTCTCTGACATCTGTTGCTACTCCCAAG 240
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Db 241 GCGCTT-GCGGACCTTTCTGGCGAGAGAAAACATATCTCTCTTGGAGGCTGTGCACTTCAAG 299
QY 320 ATGTTCTTGGGACATGAGCAATGGGTAGCGGTGAGAGACCTCTACTGCGCTTCAATGCGCTAT 379
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QY 380 GACAGGTATGTGGCCATTGTGATCTCTGAAATATATGACCCCTATAGGCCCAAGATC 439
Db 360 GACAGGTATGTGGCCATTGTGATCTCTGAAATATATGACCCCTATAGGCCCAAGATC 419
QY 440 TGTGATATATGTGGCCATCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGAT 499
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QY 500 ATGTACATATGACCT 559
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QY 560 ATCCACCCCTTGTGAGAGTGTGGCTGTGTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGAT 619
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RESULT 6
AX210248 1050 bp DNA linear PAT 31-AUG-2001
LOCUS AX210248
DEFINITION Sequence 8 from Patent WO0157215.
ACCESSION AX210248
VERSION AX210248.1 GI:15424570
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Baumgartner, J.C.
AUTHORS Radtaru, M., Spytek, K.A., Li, L., Ballinger, R.A., Mishra, V.S. and
TITLE Novel polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0157215-A 8 09-AUG-2001;
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1. 1050
Location/Qualifiers
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ORIGIN /db_xref="taxon:9606"

Query Match 85.5%; Score 835; DB 6; Length 1050;
Best Local Similarity 91.2%; Pred. No. 2.7e-237;
Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 7 AAAAAACATCATGAGAGCTCCGGAACCTCCACTTGGGAAACGGCTTCACTGTTGGG 66
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Db 119 GATTTGAATGACAGTGGGTCTCTGAACTGCTCTTATGCTATGCTTCAATCCATATAC 178
QY 127 GTTGGACATGACAGCAATGTCTGCTGCTCTGACCATACCATAGAAAGCCGGCTCA 186
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QY 187 CATGCCATGATACCTCTGCTTGGGAGCTCTCTCATATGACCTCTCTTCAATCTGT 246
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QY 367 CTTCATGGCTATGACAGGTATGTGGCCATTGTGATCTCTGAAATATGACCTCTAT 426
Db 419 CTTCATGGCTATGACAGGTATGTGGCCATTGTGATCTCTGAAATATGACCTCTAT 478
QY 427 GAGCCCAAGAGTCTGTGATCATGTGGCCACATCTGATCTCTGATCTCTGATCTCTGAT 486
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QY 547 TCTGCTGTGAGATCCACCTTGTGAGAGTGGGCTGTGATGATGATGATGATGATGATGATGATGAT 606
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QY 667 CTCTTACACTATGCTCTTATCTGCTTCTGATGATGATGATGATGATGATGATGATGATGAT 726
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RESULT 7
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LOCUS Sequence 275 from patent EP1270724.
AX646083
ACCESSION AX646083
VERSION AX646083.1 GI:28798462
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Suwa,M., Asai,K., Akiyama,Y. and Aburatani,H.
AUTHORS Guanosine triphosphate-binding protein coupled receptors
TITLE Patent: EP 1270724-A 275 02-JAN-2003;
JOURNAL National Institute of Advanced Industrial Science and Technology
(UPI), Center for Advanced Science and Technology Incubation, Ltd.
(UPI)

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CDS

ORIGIN

Query Match 85.5%; Score 835; DB 6; Length 1351;
Best Local Similarity 91.2%; Pred. No. 2.8e-237;
Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 7 AAAAAACATCATGAGAGTCCGGAATCCACTGGGAGAGGCGCTTCACTGGTGGG 66
Db 188 AAGAAACACAGATGAGAGCTCTGGAATCTGACCTGGGAGAGTGGCTTCACTTTGGTGGG 247
QY 67 GATTGAGATGAGAGGGGTCTCTGAACTGCTCTATGCTACATTACATCTTATACAT 126
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Db 308 GTTGGCCGATAGCAATGAGTGTCTGCTCTGGCCATCATCAATGAGAGCCGGCTCCA 367
QY 187 CATGCCATGATCTCTGCTGGGAGAGTCTCTCTCAATGAGAGCTCTGCTCAATCTGT 246
Db 368 CATGCCATGATCTCTGCTGGGAGAGTCTCTCTCAATGAGAGCTCTGCTCAATCTGT 427
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Db 428 TGTCACTCCCAAGGCTTGGCGGAGCTTCTGCGAGAGAAACATATCTCTTTGGAGG 487
QY 307 CTGTGACCTTCAAGTGTCTCTGCGAGTCAATGAGTGGCTGAGAGAGCTCTCACTGGC 366
Db 488 CTGTGACCTTCAAGTGTCTCTGCGAGTCAATGAGTGGCTGAGAGAGCTCTCACTGGC 547
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Db 548 CTGTGAGGCTTCAAGTGTCTCTGCGAGTCAATGAGTGGCTGAGAGAGCTCTCACTGGC 607
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Db 608 GAGCTCAAGAGCGCTGGCTGATGAGGCGACGCTCTGATCTCTGATCTCTGATTC 667
QY 487 TATGAGCATACCATGATACATATGACACCTCTCTGATGATCTCTGATGATCAAGCA 546
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Db 1148 CTAGGAGAGA 1158

RESULT 8
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DEFINITION cds, isolate:CBRCYT_386.
AB065823
ACCESSION AB065823
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S.,
AUTHORS Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y.
TITLE Genome-wide discovery and analysis of human seven transmembrane
helix receptor genes
JOURNAL Unpublished
REFERENCE Suwa,M.
AUTHORS Direct Submission
TITLE Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research
JOURNAL Center (CBRC), National Institute of Advanced Industrial Science
and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
COMMENT (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
Tel:81-3-3599-8080, Fax:81-3-3599-8081)
This sequence is a seven transmembrane helix receptor candidate
predicted from the whole human genome sequences using our automated
system that contains programs of gene
finding (GenDecoder), sequence search, motif-domain assignment and
transmembrane helix prediction.
And the sequence is submitted by the collaborative project between
[Computational Biology Research Center (CBRC), National Institute

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1723: contig of 1723 bp in length
* 1724 1823: gap of unknown length
* 1824 4819: contig of 2996 bp in length
* 4820 4919: gap of unknown length
* 4920 8082: contig of 3163 bp in length
* 8083 8183: gap of unknown length
* 8183 11955: contig of 3773 bp in length
* 11955 12056: gap of unknown length
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* 54314 54414: gap of unknown length
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* 89397 104805: contig of 15409 bp in length
* 104806 104905: gap of unknown length
* 104906 121851: contig of 16946 bp in length
* 121852 121951: gap of unknown length
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FEATURES

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ORIGIN

Query Match 85.5%; Score 835; DB 2; Length 171660;
Best Local Similarity 91.2%; Pred. No. 5.1e-237;
Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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QY 967 CTAGGAGAGA 977
 Db 79522 CTAGGAGAGA 79512

RESULT 10
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 DEFINITION AC087280
 AC087280.11 GI:17223193
 VERSION
 KEYWORDS
 HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 173611)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 JOURNAL
 REFERENCE
 AUTHORS
 2 (bases 1 to 173611)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
 Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A.,
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 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 211735)
Birren, B., Nussbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-732A19
Unpublished
2 (bases 1 to 211735)

Birren, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Bouknight, B., Brown, A., Camarata, J., Campiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Lacombe, J., Lamacz, R., Landers, T., Lenocky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Margolis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPherson, R., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougniez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talama, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 211735)

Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouknight, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sultu, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talama, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (13-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 211735)

Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouknight, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sultu, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talama, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL

Direct Submission
Submitted (03-SEP-2002) Whitehead Institute/MIT Center for Genome

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 3, 2002 this sequence version replaced gi:22123080.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: 111860

Center clone name: 732_A_19

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source

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DEFINITION	AX551020		
ACCESSION	AX551020.1		
VERSION	GI:25814025		

SOURCE ORGANISM	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
1. Alsobrook, J. P., Burgess, C. E., Grosse, W. M., Lepley, D. M., Padigaru, M. and Spytek, K. A.

TITLE
Novel single nucleotide polymorphisms for orlact
polypeptides and nucleic acids encoding the same
PATENT: WO 0236632-A 13 10-MAY-2002;
JOURNAL
Curagen Corporation (US)

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source      Location/Qualifiers
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RESULT 15

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ACCESSION AX244613
VERSION AX244613.1 GI:15859514
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Lal, P., Tang, Y.T., Patterson, C., Yao, M.G., Shih, L.H.,
Tribouley, C.M., Lu, D.A., Yue, H., Khan, F.A., Policky, J.L.,
Au-Yang, J., Yang, J., Harland, L., Walsh, R.T., Lo, T.P. and
Borowsky, M.L.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0166742-A 39 13-SEP-2001;
Incyte Genomics, Inc. (US)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2004, 13:22:47 ; Search time 101 Seconds

(without alignments)
5368.188 Million cell updates/sec

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	241	24.7	1411	4	US-09-546-986A-3
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13	226.4	22.9	966	3	US-08-748-506-6
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ALIGNMENTS

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Patent No. 5874243
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Sathe, Ganesh
TITLE OF INVENTION: NOVEL OLRC15 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY:
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,291A
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GP50001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity 57.7%; Pred No. 5.2e-84;
Matches 541; Conservative 0; Mismatches 397; Indels 0; Gaps 0;
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Db 283 AACATACACATATAGGCAAGGAGAAATGACCTTCACTCCGACTTATCTTCGGG 342
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 QY 127 GTTGGACATGACGACAAATGCTGCTGCTCTGCGGACATACCATATGAAAGCCGGCTCA 186
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 QY 187 CATGCCATGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246
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 QY 247 TGTGATCTCCAGAGGCTTGGCGGACCTTCTGCGGACGAAACATATCTCTTGGAG 306
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 QY 487 TATGACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 546
 Db 763 AATATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
 QY 547 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
 Db 823 CTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
 QY 607 GCTTATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
 Db 883 AAGGTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 942
 QY 667 CTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
 Db 943 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1002
 QY 727 AGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
 Db 1003 AGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
 QY 787 ATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
 Db 1063 GTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1122
 QY 847 TTTCTGACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 906
 Db 1123 ATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
 QY 907 GGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
 Db 1183 AGTACGACGAGATTCATGAAAGATTCAGGAAAGGCA 1220

RESULT 2
 US-08-748-506-7
 ; Sequence 7, Application us/08748506
 ; Patent No. 6159707
 ; GENERAL INFORMATION:
 ; APPLICANT: Ronnelt et al.
 ; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Voit & Mayer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: IL
 COUNTRY: US
 ZIP: 60601-6780
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/748,506
 FILING DATE: 08-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,751
 FILING DATE: 09-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 74940
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5600
 TELEFAX: 312-616-5700
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 966 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-748-506-7

Query Match 25.6%; Score 250.2; DB 3; Length 966;
 Best Local Similarity 56.1%; Pred. No. 1e-67;
 Matches 471; Conservative 0; Mismatches 368; Indels 0; Gaps 0;
 Db 117 TCTATACATGTTGGACCTGACGACGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 176
 Db 116 TCATGTTCTTATGATCTAATCAAGAAATACCTCATAGCCCTTGTCTATTTGTAACAAGTC 175
 QY 177 CCGGCTTCACATCCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 236
 Db 176 CATCTCAACACACCCCATGATCTTCTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCT 235
 QY 237 TCACATCTGTTGCTACCTCCCAAGGCTTGGCGGACTTCTGCGGAGGAAACAATATCT 296
 Db 236 ATACTGCTCTGTATACCAAGATGCTGAGACCTTGTGAGAGGCGGAGGATCT 295
 QY 297 CTTTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 356
 Db 296 CTTGGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 355
 QY 357 TCTTACTGCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
 Db 356 GCTTATGCGCAGATGCTGCTTGAACGCTATATGCTATATGTTCCCACTCCACTATG 415
 QY 417 TGACCTCATGAGCCCAAGAGTCTGCTGATCATGCTGCGGACATCTCTGATCTGAGAT 476
 Db 416 CAACTCGAATAGTCTGCGGATATGCTGCTATTTGGCAATGCTCAAGGGGATGGAT 475
 QY 477 CCTGATTTGCTATAGACATACCATGTAACATGACCTCCCTTCTGTGTGTCTGGG 536
 Db 476 GCATGATGCTGCTGCGACAGACCAATTTATTTCTCTTGAACCTCTGTGGACCTGTG 535
 QY 537 AATATGAGCATCTGCTGCTGATCCCACTGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 596
 Db 536 AGATGACCACTTCTTGTGATCTTCACTCTCTCTGCACTTCTCTGTGTGATAT 595
 QY 597 CCAAGTATGAGCTTATATATAGTGAAGGTGATCTTCTCTGTCTCCCATTTCTG 656
 Db 596 CCAAAATGAGGCTCCATCTTTGTGGAGAGAGTCTGCAATTTTGTGCAATTTTAC 655

QY 657 CCATGTGGCCCTCCACACAGTACGATCCATTCACGTGCTTCGTATGTCATCAATGAG 716
DB 656 TGAATCATTTCTTCATATGCAATTCCTGTCAGAGCTGATGATGCTTCACCTGAG 715
QY 717 GAGAGAAAGAACCCCTTCATCAGCTGCTTCCTCCACCTGATGAGTGGATGTTCTATG 776
DB 716 GAGCGCAATAAAGCTCTCTACCTGCTTCATCTCACTACTGTAAGTCACTCTTCATG 775
QY 777 GAGCTGCACATTCATGATGATCTTGGCCAGTTCCTCCACAGCCCAAGACAACA 836
DB 776 GCTCAACATTCGACACCTATTTGAGGTCTCAAGTCAAGCTCAACAGAGATGAGACAAC 835
QY 837 TCATCTGCTTTTTCACACATTCGATTCATCCAGCCCTGAATCCACTATCTACAGCTTGA 896
DB 836 TCTTGGCCCTCTTCAATACATCAGATGATCATCTGATCAATCCATCACTACAGCTTAA 895
QY 897 GGAATTAAGAGATCATGCGGCTTGAAGAGAGTCTCTGGAAATATACATCTGCTGGA 955
DB 896 GGAACAAAGAGATTAAGGATGCTGACATGAGAGAACTCTGGGCTTAAGAAAGTTCTGACA 954

RESULT 3

US-09-465-901-39
; Sequence 39, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-39

Query Match 24.9%; Score 243; DB 4; Length 669;
Best Local Similarity 60.3%; Pred. No. 1,4e-65;

Matches 402; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 210 GCGAGCTCTCTCATGAGCTCTCTGTTCACTGTTGTCATCTGCCAGGCCCTTGGCG 269
DB 2 GTCACTGTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 61
QY 270 ACTTTCGCGCAGAGAAACATATCTCTCTTGAAGCTGTGACATTCAGATGTTCTGG 329
DB 62 ATTATCTTCAAGGCAAGAGACTATTTCTTGTGGATGACACAGCTCAACACTTTCTAT 121
QY 330 CACTGCAATGGGTAGGCTGAGGACTCTCTCACTGCGCTTCATGAGCTTATGAGAGTATG 389
DB 122 ACTCAACCTGTGGAGAGCCGAGATCTTCTTCTGGGCTCAATGCTTATGATGATGATG 181
QY 390 TGGCCATTGTCTCTCTGAATAATCATGACCTCATGAGCCCAAGAGTGTGCTGATCA 449
DB 182 TGGCCATCTGCAACCCACTAGGTAACCTGTCTCATGAGCCGCGGATCTGTTGATTA 241
QY 450 TGGTGGCAATCTGATCTCTGATCTCTGATCTCTGATCTGATGATGATGATGATGATG 509
DB 242 TCAATGAGAGCTCTGATTTGGGGATCTTGTGATGATGATGATGATGATGATGATGATG 301
QY 510 TGAACCTCCCTTCTGTGTCTCTGAGGAATCAGGATCTGCTGTGAGATCCCACTT 569
DB 302 TGAGTTTCTCTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 361

QY 570 TGTGAAGTGGCCCTGTGCTGATACCTTCAGAGTATGAGCTTATATATATACGTGACAGGTG 629
DB 362 TGTGAAGTGGAGATGAGACAGACAGAGCCCTCTATGAGAGAGTATGATGATGATGATG 421
QY 630 TGAATCT 689
DB 422 TTTGATGCTGTTATCT 481
QY 690 CTGTGCTTGTGATCCATCAATGAGGAGAGAAAGCCCTGTACCTGCTCTTCC 749
DB 482 CTGTCTACATATAGCTCTGTGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541
QY 750 ACTGATTTGTGCGGATGTTCTATGAGCTGACATTCATGATGATGATGATGATGATGATG 809
DB 542 ACATGATCTGTGATACCTTGTATGAGGCTGCAATACCTATATGATGATGATGATGATG 601
QY 810 CTTTCACAGCCCAACAAAGACAAATCATCTCTGTTTCTACAAATGTCACCTGAG 869
DB 602 CTTACCAATTCCTCCATCCCAAGACAAATTTTCTGTGTTCTATACCATCTCACACCA 661
QY 870 CCTGAA 876
DB 662 TGCTGAA 668

RESULT 4

US-09-546-986A-3
; Sequence 3, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741e1 G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (118)..(1113)
; OTHER INFORMATION: human breast cancer amplified G-protein coupled
; OTHER INFORMATION: receptor 2 (BCA-GPCR-2)
US-09-546-986A-3

Query Match 24.7%; Score 241; DB 4; Length 1411;
Best Local Similarity 55.3%; Pred. No. 8.9e-65;

Matches 509; Conservative 0; Mismatches 410; Indels 2; Gaps 2;

QY 17 ATGATGAGAGTCCGGAATCCACCTTGGAGAGGCTTATCTTGTGGGATTTCTAAT 76
DB 115 ATTATGGAAGAAAGACATGCTCAATGCTTACAGGCAATTCCTGAGGCTCTTCTGAT 174
QY 77 GACAGTGGGTCTCTGTAAGTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 136
DB 175 CGGCTGAGACTGAGAAATCTCTTGTGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 234
QY 137 ACCAGATGAGTCTGCTGCTCTGCGCATACATGAGAGCCGCTGCAATGCCATG 196
DB 235 GTGAGCAACACTCCATCATCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATG 294
QY 197 TACCTCTGCTGAGAGCTCTCTCATGAGACCTCTGTTCACTCTGTTGACATGCC 256
DB 295 TACTTCTTCTGAGATCTGTTCTTATGATCTGCTTACAGCAAGATTTGCCCT 354

QY 257 AAGCCTTGGGGAATTTCGCGAGAGAAAACATATCTCTTTGGAGGCTGTGACTT 316
 Db 355 CAGCTGCTGGAACCTGGGAGGATCAGAGAAACATACCTACACAGGCTGTGGCC 414
 QY 317 CAGATGTTCTGGGCACTGACATAGGATAGCGTGAAGACTCTTACTGCGCTTCATGGCC 376
 Db 415 CAACCTATCATCTACATATGATGTGGGCTCCACGAGTGGTCTCTGTGTGATGCTCC 474
 QY 377 TATGACAGATATGTGGCCATTGTTCATCTCTGAATATCATGACCTCATGAGCCCAAGA 436
 Db 475 CATGACCCCTATGTGGCGGTCTGGCGGTCCCTGCACTACATGACATGCGCCACAT 534
 QY 437 GTCGCTGAATCATGAGGCGCAACATCTGATCTGATCCCTGATTTGCTATAGACAT 496
 Db 535 CTTCGCTGCACTGTGTACTGTGGCTGTGGTGTGTGCTGTCTTAACTCTTCATCATG 594
 QY 497 AACATGTACATATGACCTCCCTTCTGTGTGTCTGTGGAAATCAGGCATCTGCTGT 556
 Db 595 TGTCTCAGACGATCACTCTCCCGGTGTGAGCGTCCAGGGGTGACCACTTCTGTGT 654
 QY 557 GAGATCCCACTTGTCTGTAAGTGGCTGTGTGTATACC-TCAGATATGAGCTTATAT 615
 Db 655 GAGATGCTGCTCTTATTTAGCAATGCTTGTGTGAGAAACCATGTGTGAGAGCATTCAC 714
 QY 616 ATAGCTGACAGGTGTGACTTCTCTGTGTCTCCCACTTCTGCACTTGTGGCTCTACAC 675
 Db 715 CTTCGCTGAGGAGGTGGCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 773
 QY 676 ACTAGTCTATTCATCTGT 735
 Db 774 CGTATGTGACAGCGCGGT 833
 QY 736 CACCTGCTTCTTCCACCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 795
 Db 834 CACCTGCTTCTTCCACCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 893
 QY 796 TGTCTTGGCCAGTTCTTCCACGAGCCCAACAAACATCATCTCTGTTTCTACAC 855
 Db 894 CCGTGAAGCCGCGCAACAGTACTTCCCAAGATAGGAGAGTTCTTGATCTCTTCTTACAC 953
 QY 856 AATTGTCACTCCAGCCCTGATTCATCTATCTACAGCTGAGGAAATAGAGAGTCAATGCG 915
 Db 954 CATGCTCATTTCCACATCAACCCCTCATCTACCTTTGAGGAAACAGAGATGTAGAGG 1013
 QY 916 GGCCTTGAAGAGGCTGTGGG 936
 Db 1014 GACCATGAAGAAACTTGTGGG 1034

RESULT 5
 US-09-524-730-3
 ; Sequence 3, Application US/09524730
 ; Patent No. 6638733
 ; GENERAL INFORMATION:
 ; APPLICANT: Powers, Scott
 ; APPLICANT: Yang, Jianxin
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
 ; FILE REFERENCE: 018781-004710US
 ; CURRENT APPLICATION NUMBER: US/09/524,730
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1411
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (118)..(1113)
 ; OTHER INFORMATION: human breast cancer amplified G-protein coupled

; OTHER INFORMATION: receptor 2 (BCA-GPCR-2)
 US-09-524-730-3

Query Match 24.7%; Score 241; DB 4; Length 1411;
 Best Local Similarity 55.3%; Pred. No. 8.9e-65;
 Matches 509; Conservative 0; Mismatches 410; Indels 2; Gaps 2;

QY 17 ATCAGAGAGCTCCGGAACCTCCACCTTGGGAGCGGCTCATCTTGTGGGATTTCTGAAT 76
 Db 115 ATTATGGAAAGAACATGCGAGTACTTACAGGATTCATCTGTGGCTTCTGTAT 174
 QY 77 GACAGTGGTCTCTGAACTCTCTATGCAATTTACATCTTATCATGTGGACTG 136
 Db 175 CGGCTGAGACTGAGAAATTTCTTGTCTGTATCTTGATCTTGTGATCTTGTGACCTGT 234
 QY 137 ACCAGCAATGCTGTGCTGCTCTGCGCCATCAACATAGAAAGCCGCGTCCATGCGCAT 196
 Db 235 GTGGCAACACTGCGCATATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 294
 QY 197 TACCTCTGCTTGGGCAAGCTCTCTCATGAGACCTCTGTTCACTGTGTGCACTCC 256
 Db 295 TACTTCTTCTTGGGAATCTGTCTTTTATGATCTGTCTTTACAGCAAGCATTGCCT 354
 QY 257 AAGCCTTGGGGAATTTCGCGAGAGAAAACATATCTCTTGTGAGGCTGTGACTT 316
 Db 355 CAGCTGCTGGAACCTGGGAGGATCAGAGAAACATACCTACACAGGCTGTGGCC 414
 QY 317 CAGATGTTCTGGGCACTGACATAGGATAGCGTGAAGACTCTTACTGAGCTTCAATGGCC 474
 Db 415 CAACCTATCATCTACATATGATGTGGGCTCCACGAGTGGTCTCTGTGTGTGTGTGT 534
 QY 475 CATGACCGCTATGTGGCGGTCTGTGCGGTCTGTGACATAGGAGATGTGGCCACAT 594
 Db 535 CTTCGCTGCACTGTGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 675
 QY 594 497 AACATGTACATATGACCTCCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 735
 Db 735 774 CGTATGTGACAGCGCGGT 833
 QY 736 CACCTGCTTCTTCCACCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 795
 Db 795 834 CACCTGCTTCTTCCACCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 893
 QY 834 856 AATTGTCACTCCAGCCCTGATTCATCTATCTACAGCTGAGGAAATAGAGAGTCAATGCG 915
 Db 915 954 CATGCTCATTTCCACATCAACCCCTCATCTACCTTTGAGGAAACAGAGATGTAGAGG 1013
 QY 954 916 GGCCTTGAAGAGGCTGTGGG 936
 Db 936 1014 GACCATGAAGAAACTTGTGGG 1034

RESULT 6

```

US-08-748-506-8
; Sequence 8, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Romnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-748-506-8

Query Match      24.3%; Score 237.4; DB 3; Length 966;
Best Local Similarity 55.2%; Pred. No. 9.5e-64;
Matches 463; Conservative 0; Mismatches 376; Indels 0; Gaps 0;

QY 117 TCCTAATCATGTGGCACTGACCAAGCATGCTGCTGCTGCGCATCACCATAAG 176
DB 116 TCATGTTCTTAGTATCACTAACAGAAATGCTTCATAGCCCTTGCTATTGTACAGATC 175
QY 177 CCGGCTCCACATGCCCATGTACTCTGCTTGCGGAGCTCTCTCTCATGAGCCTCTGT 236
DB 176 CATCTCTACACACCCCATGTACTCTCTTGCGCAACTGTCTCTCTGAGATTGGCT 235
QY 237 TCACATCTGTGACTGCCCAAGGCTTGCGGAGCTTCTGCGCAAGAAACACTATCT 296
DB 236 ATACTGCTCTGTATACCAAGATGCTGCAAGCTCTTGTAAGAGAGGCCGAGAGATCT 295
QY 297 CTTTGGAGGCTGTGCACTTCAGATGTTCTCTGCACTGACATGGGTAGCGCTGAGACC 356
DB 296 TTGAGGTGGATGTGCGCACAGATGTTTTCTTCATATTTCTTTGATTAATGATGCT 355
QY 357 TCTACTGGCTTATGAGCTTATGACAGATATGTGGCCATTTGTGATCTTGAATACA 416
DB 356 GCTTATTTGGCAGCATGGCTTTGACCGCTATATGCTATATGTTCCCACTCCACTATG 415
QY 417 TGACCTCATGAGCCCAAGAGTCTGCTGAGATCATGAGTGGCCACATCCGATGATCTGGAT 476
DB 416 CAACCCGATAGTGTGAGGTATGTGCGCACTTGCGCAATTTGTTCAATGGGTGAT 475
QY 477 CCTGATTTGCTATAGACATACATGTACACTATGACCTCTTCTGTGTGCTGCGG 536
DB 476 GCATAGTATGCTGTGGGACAGACCAATTTATTTCTCTTGAACCTTCTGTGAGACCTGTG 535

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QY 537 AATCAGCATCTCTCTGTGAGATCCACCTTGTGCAAGTGTGCTGTGATTA 596
DB 536 AGATGACCACTTCTCTGTGATCTTCCACTTGTGCACTTGTGCTGTGATTA 595
QY 597 CCAGTATGAGCTTATATAGCTGACAGGTGACCTTCTCTGTGCTGCCATTTG 656
DB 596 CCAATTTGAGGCTGCACTTCTTGTGAGTGTCTCTGTGATATCTAGCCCTTTTTC 655
QY 657 CCATTTGGCTCTCTACACACTAGTCTTATCTAGTGTCTGATGCAATGAG 716
DB 656 TGATCATTTATTTTATGATGAGATTTCTGTGAGTGTGTATGCTTCACTGAG 715
QY 717 GGAGAAAGAAAGCCCTTGTACCTGCTTCTTCCACTGATTTGTGTGGAGTTTATG 776
DB 716 GGCCGCAAGAGCCCTTCAACTGTTCTTCCACTACTATTTAGTACACTCTTTATG 775
QY 777 GAGTGCACATTCATGATGTCTTGCCCGCTTCTTCCAGGCCCAAGCAAGAC 836
DB 776 GCTAGGATCTTTACTATTTGAGGCTTAACTTACCTCTACACAGAAATGACAAAC 835
QY 837 TCATCTGTTTTTACACATTTGTCACTCCAGCCCTGAATCCATCTTACAGCCTGA 896
DB 836 TCTTGCCCTCTTACACAGACATGATCATGTTGAACCTTATCATATGTTAA 895
QY 897 GGATTAAGAGGTATGCGGCTTGTGAGAGGCTCTGGAAATTAATCACTGCTGGA 955
DB 896 GGAACAAGATGTACAGCAGCACTGAGAAATTTGCGCCCTGAAAAAATTCGTCA 954

RESULT 7
US-08-748-506-5
; Sequence 5, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Romnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-748-506-5

Query Match      24.3%; Score 237; DB 3; Length 966;
Best Local Similarity 55.1%; Pred. No. 1.3e-63;

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Matches 462; Conservative 0; Mismatches 377; Indels 0; Gaps 0;

QY 117 TCCTATACATGTTGGACCTGACACCAATGTCGTCTGTCCTGGCCATCACCATAAG 176
 Db 116 TCATGTTCTTAACTACATACAGAAATACTCTATAGTCCTGCTATTGTTACCACTC 175
 QY 177 CCCGCTCCACATGGCCATGATGCTCTGCTGGAGCTCTCTCATGACCTCTGT 236
 Db 176 CATCTCTACACACCCCATGATGCTCTCTGGCCAACTGTCCTCTGGAGATTGGT 235
 QY 237 TCACATCTGTTCTACTCCCAAGCCCTGGGCACTTTCTGGCAGAGAAAACATAT 296
 Db 236 ATACTGCTCTCTCACTACCAAGATGCTGACAGCCCTTGTGATGAGGCAAGATCT 295
 QY 297 CTTTGGAGGCTGTGACCTTCAATGTCCTGGCACTGACAAATGGGTAGCGTGAGACC 356
 Db 296 CTGGGAGGATGTGACACAGATGTTTTTTTGGCATTTTTTGGTAACTGAGTGT 355
 QY 357 TCCTACTGGCTTCATGGCCCTATGACAGGTATGAGCCATTGTGATCTCTGAATAACA 416
 Db 356 GCTATTTGGCAGCATGGCTTTGACCGCTGATGAGCCATATGCTCCCACTCACTATG 415
 QY 417 TGACCTCTATGAGCCCAAGATGCTGTGATGATGATGAGCCATCTGATCTGGCAT 476
 Db 416 CAACCCGATGATGAGGATGATGAGCCATTTGGCAATTTTCAATGGGAAATGGGAT 475
 QY 477 CCTGATTTCTTAAAGACATACCATGATACATATGACATCCCTCTGTCGTCTGAG 536
 Db 476 GATATGATGATCTGGGACAAACCAATTTATTTCTCTGTAACCTTCTGAGACCTGTG 535
 QY 537 AATCAGGATCTGCTGTGAGATCCCACTGTGTAAGTTGGCTGTGTCATACCT 596
 Db 536 AATATGACACATTTCTGTGACCTTCCACTCTCTGACATCTGCTGTGAGATACAT 595
 QY 597 CCAAGTATGATCTTAAATATAGTACAGGTGTGACTTCTCTGCTGCCCATTTCTG 656
 Db 596 CCAAAACAGAGCTGTGACATCTTGTGTGAGTGTGATCTGATCTACATCCCAATTTTGC 655
 QY 657 CCATTTGGCTCTCTACACATGATCTTATTCATGCTGTGCTGTGATGACCAATAGAG 716
 Db 656 TGATCATTTATTTCTTATGTCAAATTTCTATGCTGATGCTGATGCTTCACTGAGG 715
 QY 717 GAGAGAGAGAGCCCTGTGACCTGTCTTCCACCTGATGTTGTGAGGATGTTCTATG 776
 Db 716 GGGCGCATTAAGCTCTTCCACCTGTGTGCTCACTACTTGAATGACACTTTTTTATG 775
 QY 777 GAGCTGCACTTATGATGTTCTTGGCCAGTTCTTCCACAGCCCAACAAAGACACA 836
 Db 776 GCTCAGCATGATTAATCTTATTTGAGGCCCAAGCTTAGCCATCACCAGGATGACAAAT 835
 QY 837 TCATCTCTGTTTCTACACATTTGTCACCTCCAGCCCTGAATCCATCTACAGCTGA 896
 Db 836 TCTTGCCCTCTTCTACAGATGATGATCTGATGATGATGATGATGATGATGATGAT 895
 QY 897 GGAATTAAGAGATGATGAGGCTTGGAGAGGCTCTGGGAAAATACATATGCTGGCA 955
 Db 896 GGAACAAAGAGATGAGGAGGACTGAGAAACTGTGGGCTGAAAAAATTTCTGCA 954

RESULT 8
 US-09-546-986A-7
 ; Sequence 7, Application US/09546986A
 ; Patent No. 6635741
 ; GENERAL INFORMATION:
 ; APPLICANT: Powers, Scott
 ; APPLICANT: Yang, Jianxin
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: Tularek Inc.
 ; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
 ; FILE REFERENCE: 018781-004720US
 ; CURRENT APPLICATION NUMBER: US/09/546, 986A
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 09/524, 730

PRIOR FILING DATE: 2000-03-14
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 1065
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (26)..(1030)
 ; OTHER INFORMATION: human breast cancer amplified G-protein coupled
 ; OTHER INFORMATION: receptor 4 (BCA-GPCR-4)
 US-09-546-986A-7

Query Match 23.8%; Score 232.4; DB 4; Length 1065;
 Best Local Similarity 53.8%; Pred. No. 3.6e-62;
 Matches 479; Conservative 0; Mismatches 411; Indels 0; Gaps 0;

QY 50 GGCTTCATCTTGGTGGGGAATCTGAATGACAGTGGGTCTCTGAACGTCTATGCTACA 109
 Db 116 GGTTCATCTTGTAGGGTTTCTGATTAATGCTAGTACAGAGATCTATTTGTGCTC 175
 QY 110 TTTAACATCTTATCATGTTGGACATGACAGCATATGCTCTGCTCTGACCATCAC 169
 Db 176 ATATTGATTTCTGATTTACTTAATTTTGGGAAATACCAACATATCTGTTCTGCT 235
 QY 170 ATGAGAGCCCGCTCCACATGAGCCATGATACCTCTGCTTGGGAGCTCTCTCATAGAC 229
 Db 236 CTGGAACCAAGCTTCATATGCGCATGATATTTCTTCTTCTCATCTCTCTCTGATAC 295
 QY 230 CTCTGTTCACTCTGTTGTCTACCTCCAGAGCTTGGCGGACTTCTGCGCAGAGAAAC 289
 Db 296 CGCTCTTACACAGCAGATGTTATCTCCAGCTCTGTTAACTGTGGAGAACCAATGAAA 355
 QY 290 ACTATCTCTTGGAGGCTGTGACATTCAGATGTTCTGAGCACTGACATGGGTAGCGCT 349
 Db 356 ACTATGCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 415
 QY 350 GAGAGCTCTCTACAGGCTCTTATGAGCTATGACAGGATGAGGACATTTGTATCTCTG 409
 Db 416 GAGTGGCTCTCCGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
 QY 410 AATATCAGTACCTTATGATGAGCCCAAGAGCTGTGATGATGATGATGATGATGATGAT 469
 Db 476 CATTAACATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535
 QY 470 CTGGATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
 Db 536 AGTGAATAGCCACACACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
 QY 530 TCTGGGAAATCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 589
 Db 596 CATGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655
 QY 590 GATACCTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
 Db 656 GGCACACAGTTTAAGAGGCTGAGCTTTTGTGCTAGATCTTTTCTTTATGAGCTT 715
 QY 650 ATTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 709
 Db 716 GTCTATTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 775
 QY 710 AATGAGGAGGAGAAAGCCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 769
 Db 776 GCTACCGGAGAGACAAAGCATTTGGGAGCTGCTTCTCCACTGACAGTGTGACACATC 835
 QY 770 TTCTATGAGCTGACATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 829
 Db 836 TTTTATGAAACATCATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895
 QY 830 GACACATATCTGTTTCTTACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 889
 Db 896 GGCAGTGTGTTCTCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955

QY 890 AGCCGAGGAAATAGAGAGTCATGCGGCTTTGAGAGGCTCTGGAAA 939
DB 956 ACCTTGAGATCAAGAGAGTGAAGAGGCAATTAAGAAAGTTCTAGCAA 1005

RESULT 9

US-09-524-730-7
Sequence 7, Application US/09524730
Patent No. 6638733
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
FILE REFERENCE: 018781-004710US
CURRENT APPLICATION NUMBER: US/09/524,730
CURRENT FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1065
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (26)..(1030)
OTHER INFORMATION: human breast cancer amplified G-protein coupled
OTHER INFORMATION: receptor 4 (BCA-GPCR-4)
US-09-524-730-7

Query Match 23.8%; Score 232.4; DB 4; Length 1065;
Best Local Similarity 53.8%; Pred. No. 3.6e-62;
Matches 479; Conservative 0; Mismatches 411; Indels 0; Gaps 0;

QY 50 GGCTCATCTTGGGGGATTCGAATGACAGTGGGTCTCTGACAGCTCTATGCTACA 109
DB 116 GGTTTCATCTTTAGGGTTTCTGATTAAGCTAGTTACGAAGGTTCTATTGTGCTC 175
QY 110 TTACATCTTATCATATGTTGGACATGACACGACATGGTCTGCTCTGGCCATCAC 169
DB 176 ATATTGATTTGTAATTTACTAATATTTGGGAATACACATCATCTTGTTCTGCT 235
QY 170 ATAGAACCGGCTCCACATGATGATCTCTGCTGGGAGCTCTCTCATGAGAC 229
DB 236 CTGGAACCCAAAGCTTCAATGACGATGATTTCTTCTTCTCATCTCTCTCTGAC 295
QY 230 CTCTCTTCATCTGTGTGCTACCTCCCAAGGCTTGGCGGATTTCTGCGGAGAAAAC 289
DB 296 CGCTGCTTACACAGAGTGTATTCCTCCAGCTCTGTGTAACCTGTGGAAACCATGAAA 355
QY 290 ACTATCTCTTTGAGGCTGTGCACTTCAGATGTTCTTGGACATGACATGGGTAGGCT 349
DB 356 ACTATGCTCTATGTTGCTGTTGTTGTTCACTTTACAACTCCATGCTTGGGATCCACT 415
QY 350 GAGACCTCTACTGCGCTTCAAGGCTTATGACAGGTATGTGGCAATTTGTCATCTCTG 409
DB 416 GAGTGCCTCTCCCGGCTGATGATCTGTAACCGATATGAGCTGTGCGCTCTCTC 475
QY 410 AATATCATGACCTTCATGAGCCCAAGATCTGCTGATCATGTGGGCAATCTGTGATC 469
DB 476 CATTAAGCTGTCTTAAGCATATTCATCTGCAATGAGCTTGGGATCTATGGCATGGCTC 535
QY 470 CTGGCATCTCTGATTGCTATAGACATACATGATACATGACATCTCCCTTCTGTGTG 529
DB 536 AGTGAATAGCAACCACTGTGTACAGTCCACCTTCACTGACGCTGCTCTTCTGTGGG 595
QY 530 TCTGGGAAATCAGGATCTGCTGTGAGATCCACCTTGTGAAATTTGGCTGTGCT 589
DB 596 CATGCCAAGTGAATCTTTCATCTGCAAGGCTCTGCTGCTCATCAAGCTGGCTTGTGTG 655
QY 590 GATACCTCCAGGATGAGCTTATATATATAGTGAAGAGTGTGACTTCTCTTCTGCTCCC 649

DB 656 GGACCAAGTTTACAGAGGCTAGCTTTTGTGCTAGTATCTTTCTTATAGTGCTT 715
QY 650 ATTTCGCAATTTGAGGCTCTTACACATGATCTTATCTAGTCTGTATGCTATCA 709
DB 716 GTCTCATTCATCCGTGCTCTCTCTGCTACATTCGCCAGAGTGTAGATTAAGTCA 775
QY 710 AATGAGGAGGAAAGAAAGCCCTTGTCACTGCTCTTCCACCTGATTTGCTGGAGTG 769
DB 776 GCTACCCGGAGACAGAAAGCATTTGGGACCTGCTTCCACCTGACAGTGTGATCACATC 835
QY 770 TTCTATGAGCTGCAATTCATGATGTCTGTGCGCAGTTCCTCCACAGCCCAAGAA 829
DB 836 TTTATGAAACCATCATCTTATGATGTCTGCAAGCCCAAGAGTATGATCCAGGACCA 895
QY 830 GACAACATCATCTCTGTTTCTTACACATTTGTCACTCCAGCCCTGAATTCATCTAC 889
DB 896 GGCAAGTTGTTTCTCTCTTCTTACATGCTGTGAACCCGACATCTTAACCTCTTATTTAT 955

QY 890 AGCCTGAGAAATAAGAGTCAATGCGGCTTGAAGAGGCTCTGGGAAA 939
DB 956 ACCTTGAGATCAAGAGGTCGAAGGGGCAATTAAGAAAGTTCTAGCAA 1005

RESULT 10

US-09-016-434-1115
Sequence 1115, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE//DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1115:
SEQUENCE CHARACTERISTICS:
LENGTH: 952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1336042
US-09-016-434-1115

Query Match 23.6%; Score 230.4; DB 4; Length 952;

Best Local Similarity 54.7%; Pred. No. 1.4e-61;
Matches 499; Conservative 0; Mismatches 411; Indels 2; Gaps 2;

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QY 32 AACTCCACCTTGGAGAGGGCTTATCTTGGTGGGGATTTGGAATGACAGTGGCTCTCT 91
Db 13 AACACAGACTTGGGTAGAGAAATTAATTTCTCCGGCCCTGACAGCTGGAGACCTGG 72
QY 92 GAACGTCTTATGACATTTACATCTTATACATGTTGGGACCTGACAGCAATGGTCTG 151
Db 73 GTCCTCCCTGTTTGGTCTTCTTGGTCTATGATGAGAGCCGTGCTGGGAACTGTCTC 132
QY 152 CTGCTCTGGCCATCAGCAATGAGAGCCCGCTCCATGCTCCATGCTCTCTGCTGG 211
Db 133 ATGTCCTTCTGATCAGATGAGAGCCGAGCTCCACATCCCATGATATTTCTTCTCAC 192
QY 212 CAGCTCTCTGATGAGACCTCTGTTACATCTGTTGACATCTGTTGACCTCCCAAGCC 271
Db 193 AACCTCTCCCTGATGATGATCTCTATGACCAAGTATGTCCTCCACCTGCTGGACAT 252
QY 272 TTTCTGCGCAGAGAAACACTATCTCTTGGAGGCTGACATTCAGATGTTCTGGCA 331
Db 253 TTTCTGAGAGAACTAAGAGCCATCCCATTCAGAGCTGTGACGCCCACTATTTTCTCC 312
QY 332 CTGACATGAGGTAGGCTGAGAGACCTCTACTGCTTATGAGCTTATGACAGTATG 391
Db 313 CTGGCCTTGGGTGGATGATGATTTGTTCTCT - GCGGTATGAGCTTATGACCGTATG 371
QY 332 GGCATTTGATCTCTGTAATAATACATGACCTCAGATGAGCCCAAGAGTGTGATG 451
Db 372 GGTGATGATGAGCCCT - GATATCTGGGCAATGACATGAGAGGCTGTGTGATG 430
QY 452 GTGGCAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 511
Db 431 GGCATCAATCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 490
QY 512 CACCTCTCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 571
Db 491 CAGCTGCGCATGAGAGAAACAAGTTTATGATCAATCTGATGATCTGATGATCTG 550
QY 572 CTGAGATGAGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 631
Db 551 GTCAGGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 610
QY 632 ACTTCTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 691
Db 611 GTTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 670
QY 692 GTGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 751
Db 671 ATCTAAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 730
QY 752 CTGATGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 811
Db 731 CTCAAGAGTGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 790
QY 812 TTCCACAGCCCAACAAGACAATCATCTCTGTTTCTACACATTTCTACCTCAGCC 871
Db 791 AGTCCCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 850
QY 872 CTGAATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 931
Db 851 CTGAAGCCCATGATTTACAGCTTAAGAGATTAAGAGGTGAGAGGCGCTGGAGAACTA 910
QY 932 CTGGGAAATAC 943
Db 911 TTATGAAATTC 922

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RESULT 11
US-09-546-986A-1
; Sequence 1, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:

```

; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cuflet, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)..(974)
; OTHER INFORMATION: human breast cancer amplified G-protein coupled
; OTHER INFORMATION: receptor 1 (BCA-GPCR-1)
; US-09-546-986A-1

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Query Match 23.4%; Score 228.4; DB 4; Length 1035;
Best Local Similarity 55.0%; Pred. No. 6.2e-61;
Matches 448; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

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QY 122 TACATGTTGGACATGACAGACCAATGCTGCTGCTCTGAGCCATACCAATGAGCCGG 181
Db 135 TATGCTGAGCCATGTTGGAGAACCTCCCATCATCTGAGCATCCGGGTGATCTTCAA 194
QY 182 CTCCACATGACCCATGATGATCTCTGTTGGAGAGCTCTCTCATGAGACCTCTGTTCA 241
Db 195 CTCCACAGCCCATGATGATCTCTCTGATGATCTGATGATCTGATGATCTGATGAT 254
QY 242 TCTGTTGATCTCTCCAAAGCCCTTGGAGAGCTTTCTGCGCAGAGAAACATATCTCT 301
Db 255 ACCAGAGAGTCCCTCAATGCTGATGATGATGATGATGATGATGATGATGATGAT 314
QY 302 GAGAGCTGACATCTGATGATCTGATGATCTGATGATCTGATGATCTGATGATCTG 361
Db 315 GAGAGCTGATCTGATGATCTGATGATCTGATGATCTGATGATCTGATGATCTGAT 374
QY 362 CTGGCCTTCAATGAGCCATGATGATGATGATGATGATGATGATGATGATGATGAT 421
Db 375 CTGGCCTTCAATGAGCCATGATGATGATGATGATGATGATGATGATGATGATGAT 434
QY 422 CTGATGAGCCCAAGAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 481
Db 435 CTGATGAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 494
QY 482 ATGCTATGAGACATACCATGATGATGATGATGATGATGATGATGATGATGATGAT 541
Db 495 AACTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 554
QY 542 AAGCATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
Db 555 AACCACTTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 614
QY 602 TATGAGCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
Db 615 AATGACACCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 674
QY 662 GTGGCCTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721
Db 675 CTCTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 734
QY 722 AAGAAAGCCCTTGTACCTGCTCTTCCACCTGATGATGATGATGATGATGATGAT 781
Db 735 CACAAGGCTTTGGAGAGGTGCTCTCCACCTGATGATGATGATGATGATGATGAT 794
QY 782 GCCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 841

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Db 795 GCGATTACATGATATCTGAGCCCCCTTCAGTACTCCCAAGAGGGAATTAT 854
QY 842 TCTGTTTCTACAAATGTCATCTCGAGCCCTGAAATCCATGATTAAGCCTGAGAA 901
Db 855 TCTCTCTTCTATTCATATCAACCCCTCACTCTCAATCCCTTACCTACACCTGAGAA 914
QY 902 AAGAGGTGATGCGGCGCTTGAGAGGGTCTCG 935
Db 915 AAAGTATGAAAGGGGCTCTGAGAGGACTTCTGG 948

RESULT 12

US-09-524-730-1
Sequence 1, Application US/09524730
Patent No. 6638733
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. 6638733el G-Protein Coupled Receptors
FILE REFERENCE: 018781-004710US
CURRENT APPLICATION NUMBER: US/09/524,730
CURRENT FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1
LENGTH: 1035
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (42)..(974)
OTHER INFORMATION: human breast cancer amplified G-protein coupled
US-09-524-730-1

Query Match 23.4%; Score 228.4; DB 4; Length 1035;
Best Local Similarity 55.0%; Pred. No. 6.2e-61;
Matches 448; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

QY 122 TACATGTTGGCACTGACGACCAAGATGTCGTGCTCTCGGCAATCAGCATAGAACCCGG 181
Db 135 TATGTGCTGGCAATGTTGGGAAAGTGGCCATCATCTGGATATCCGGGTGATCTTCAA 194
QY 182 CTCACATGCCCCATGTACTCTGCTTGGGAGCTCTCTCATGAGACTCTGTTACA 241
Db 195 CTCACAGCCCCCATGTAATCTTCTGATCACTGTCCTTCTGGAGCTCTGTTACACC 254
QY 242 TCTGTTGTCATCTCCCAAGGCTTGGCGGACTTTCGCGCAGAGAAAACATATCTCTT 301
Db 255 AACACGACAGTCTCCCTGATGCTGTCACATGAGGAGTTCCGAGAAACATAGCTAT 314
QY 302 GAGGCGTGTGCACTTGCATGATGTTCTGGCACTGACATAGGAGTGGCGTGAAGCTTCT 361
Db 315 GAGGCGTGTGCACTGATGATGATGATGCTTTCATCTGCGTGGAGTGAAGAGTGTGTC 374
QY 362 CTGGCTTCAATGAGCTATGACAGGTATGAGGCAATTTGTCATCTTGAATACATGACC 421
Db 375 CTGGCGGCAATGAGCTTGAAGCGGTAGTGGCAGAGCTGCAAGCCCTGACATAGCCGT 434
QY 422 CTGATGAGCCCAAGAGTCTGCTGATCATGTTGGCCACATCTGATCTGGCAATCCCTG 481
Db 435 CTGATGAGCCGCTCTCTGTCAGACAGCTGTGCTTGGCTGAGCTCACTGAGCTTGGC 494
QY 482 ATTGCTATAGGACATACATGATGATGATGATGATGATGATGATGATGATGATGATG 541
Db 495 AACTCTCTGCTGAGAGTGTGCTGAGAGTGTGATGATGATGATGATGATGATGATGATG 554
QY 542 AGGCAATCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 601
Db 555 AACCACTTTTCTGTAGAGTGTGCGGCGGTGATCATAGCTGTGATGATGATGATGATG 614

QY 602 TATGACTTATATATATGATGACAGTGTGACTTTCCTCTGCTCCCATTTTCGCCANT 661
Db 615 AATGACACCATATCTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 674
QY 662 GTGCGCTTCTACACATAGTCTTATCATCTGTGCTGTGATGATGATGATGATGATGATG 721
Db 675 CTCTCTCTATGAGCTTATATGCCCCGAGTGTGATGATGATGATGATGATGATGATGATG 734
QY 722 AAGAAAGCCCTTGTACCTGCTCTTCCCACTGATGATGATGATGATGATGATGATGATG 781
Db 735 CACAAGGCTTTGGAGAGTGTCTCTCCCACTGATGATGATGATGATGATGATGATGATGATG 794
QY 782 GCGACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 841
Db 795 GCGATTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 854
QY 842 TCTGTTTCTACAAATGTCATCTCGAGCCCTGAAATCCATGATTAAGCCTGAGAA 901
Db 855 TCTCTCTTCTATTCATATCAACCCCTCACTCTCAATCCCTTACCTACACCTGAGAA 914
QY 902 AAGAGGTGATGCGGCGCTTGAGAGGGTCTCG 935
Db 915 AAAGTATGAAAGGGGCTCTGAGAGGACTTCTGG 948

RESULT 13

US-08-748-506-6
Sequence 6, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voie & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: 74940
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-6

Query Match 23.2%; Score 226.4; DB 3; Length 966;
Best Local Similarity 54.2%; Pred. No. 2.5e-60;
Matches 455; Conservative 0; Mismatches 384; Indels 0; Gaps 0;

QY 117 TCTTATACATGTTGGACGACGACGATGATGATGATGATGATGATGATGATGATGATG 176

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signal processing.

PS Claim 8; Page 10; 111bp; English.

CC The present sequence is that of a nucleic acid encoding a novel human G-protein coupled receptor, designated GPCR1, that has structural and physiological functions characteristic of the olfactory receptor family. CC The invention provides GPCR1 polypeptides, nucleic acids and antibodies. CC These are useful for treating or preventing a GPCR1-associated disorder, such as cardiomyopathy, atherosclerosis, diabetes, or a disorder related to cell signal processing or metabolic pathway modulation in humans CC (claimed). They may further be used for treating or preventing e.g. developmental diseases, metabolic pathway disorders, retinal disorders, wasting disorders associated with chronic diseases, pain, cancer, psychotic and neurological disorders (e.g. anxiety or schizophrenia), autoimmune diseases, allergies, bacterial, fungal, protozoal and viral infections, neurodegenerative diseases (e.g. Alzheimer's disease), and haematopoietic diseases. The proteins and nucleic acids may also be used as research tools, as diagnostic or prognostic markers, in gene therapy, for promoting tissue regeneration in vitro and in vivo, and as biological defence weapons. The nucleic acids may also be used in chromosome mapping, in tissue typing, in forensic biology (e.g. to identify individuals from minute biological samples), in forensic identification of a biological sample, as surrogate markers, and in pharmacogenomics

XX Sequence 977 BP; 215 A; 279 C; 220 G; 263 T; 0 U; 0 Other;

Query Match 100.0%; Score 977; DB 6; Length 977;
Best Local Similarity 100.0%; Pred. No. 4.1e-285;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACTAAAAAACAATCATGAGAGCTCCGAACTCCACCTTGGGAAAGCGCTTCATCTT 60
DB 1 GCAACTAAAAAACAATCATGAGAGCTCCGAACTCCACCTTGGGAAAGCGCTTCATCTT 60
QY 61 GGTGGGAGATTCTGAATGACAGTGGGCTCTCTGAACTCTTAATGCTTAACTTAACTTCT 120
DB 61 GGTGGGAGATTCTGAATGACAGTGGGCTCTCTGAACTCTTAATGCTTAACTTAACTTCT 120
QY 121 ATACATGTTGGACATGACACCAATGATGCTGCTGCTGGGCATCAACATGAAAGCCG 180
DB 121 ATACATGTTGGACATGACACCAATGATGCTGCTGCTGGGCATCAACATGAAAGCCG 180
QY 121 ATACATGTTGGACATGACACCAATGATGCTGCTGCTGGGCATCAACATGAAAGCCG 180
DB 121 ATACATGTTGGACATGACACCAATGATGCTGCTGCTGGGCATCAACATGAAAGCCG 180
QY 181 GCTCCACATGCGCATGATGCTGCTGCTGGGAGCTCTCTCAATGACCTCTGTTTAC 240
DB 181 GCTCCACATGCGCATGATGCTGCTGCTGGGAGCTCTCTCAATGACCTCTGTTTAC 240
QY 241 ATCTGTTGCTACTCCCAAGGCTTGGGCGACTTTTGGCGAGAGAAAACATATCTCTT 300
DB 241 ATCTGTTGCTACTCCCAAGGCTTGGGCGACTTTTGGCGAGAGAAAACATATCTCTT 300
QY 301 TGGAGGCTGTGACATTCAGATGTTCTTGGCACTGACATGAGGATGAGGAGACCTCT 360
DB 301 TGGAGGCTGTGACATTCAGATGTTCTTGGCACTGACATGAGGATGAGGAGACCTCT 360
QY 301 TGGAGGCTGTGACATTCAGATGTTCTTGGCACTGACATGAGGATGAGGAGACCTCT 360
DB 301 TGGAGGCTGTGACATTCAGATGTTCTTGGCACTGACATGAGGATGAGGAGACCTCT 360
QY 361 ACTGACCTTCAATGAGGCTTGAAGGATGATGAGGATGATGAGGATGATGAGGATGAT 420
DB 361 ACTGACCTTCAATGAGGCTTGAAGGATGATGAGGATGATGAGGATGATGAGGATGAT 420
QY 421 ACTGACCTTCAATGAGGCTTGAAGGATGATGAGGATGATGAGGATGATGAGGATGAT 480
DB 421 ACTGACCTTCAATGAGGCTTGAAGGATGATGAGGATGATGAGGATGATGAGGATGAT 480
QY 481 GATTGCTTATGAGCACTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 GATTGCTTATGAGCACTTACATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 CAGGATCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 CAGGATCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GTATGAGCTTAT 660
DB 601 GTATGAGCTTAT 660

QY 661 TGTGGCTCTCTACACACTAGTCTTATCTAGTCTTGTATGATGATGATGATGATGATGAT 720
DB 661 TGTGGCTCTCTACACACTAGTCTTATCTAGTCTTGTATGATGATGATGATGATGATGAT 720
QY 721 GAAAGAAAGCCCTTGTACACTGCTCTTCCACCTGATGATGATGATGATGATGATGATGAT 780
DB 721 GAAAGAAAGCCCTTGTACACTGCTCTTCCACCTGATGATGATGATGATGATGATGATGAT 780
QY 781 TGGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 TGGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 CTCTGTTTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 CTCTGTTTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 TAAAGAGTCAATGAGGAGCTTGAAGAGGATGATGATGATGATGATGATGATGATGAT 960
DB 901 TAAAGAGTCAATGAGGAGCTTGAAGAGGATGATGATGATGATGATGATGATGATGAT 960
QY 961 CAGGCTCTAGGAAAGGA 977
DB 961 CAGGCTCTAGGAAAGGA 977

RESULT 2

AAH31857 standard; DNA; 947 BP.

AAH31857; 30-JUL-2001 (first entry)

Human olfactory receptor polynucleotide, SEQ ID NO: 430.

Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation; ds.

Homo sapiens.

MO200127158-A2.

19-APR-2001.

06-OCT-2000; 2000MO-US027582.

08-OCT-1999; 99US-0158615P.

24-FEB-2000; 2000US-0184809P.

(DIGI-) DIGISCENTS.

(YEDA) YEDA RES & DEV CO LTD.

Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

WPI; 2001-290713/30.

New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.

Claim 8; Page 352; 1857bp; English.

The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a

CC neuronal tissue, in production of transgenic plants and for the
 CC development of new drug targets for various disorders. This sequence
 CC represents DNA encoding a human OR protein

XX Sequence 1050 BP; 234 A; 293 C; 238 G; 285 T; 0 U; 0 Other;

Query Match 85.5%; Score 835; DB 5; Length 1050;
 Best Local Similarity 91.2%; Pred. No. 4,4e-242;
 Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

```

QY 7 AAAAAACACATCATGAGCTCCGAACTCCACTTTGGGAAAGCGCTTCATCTTGCGG 66
DB AAGAAACACACGATGAGCTCTGAACTTCACCTTGGAAGTGGCTTCATTTGGG 118
QY 67 GATCTGAATGAGTGGGTCTCTGAACTGCTATGATCAATTTCAATCTATACAT 126
DB 119 GATTTGAATGAGTGGGTCTCTGAACTGCTCTGAACTGCTCTGAACTTACTT 178
QY 127 GTTGGCACTGACGACGATGGTCTGCTGCTCTGCGCATACATAGAGCCGCTCCA 186
DB 179 GTTGGCCCTGATGACGATGGCTCTGCTCTGCTATGACATGGAAGCCGCTCCA 238
QY 187 CATGCCATGATGATCTCTGCTGGGAGCTCTCTCTCATGAGACCTCTGTTCAATCTGT 246
DB 239 CATGCCATGATGATCTCTGCTGGGAGCTCTCTCTCATGAGACCTCTGTTCAATCTGT 298
QY 247 TGTGACTCCGAGGCGCTTGGGGAAGCTTCTGCGAGAGAAACATATCTGCTTGGAG 306
DB 299 TGTGACTCCGAGGCGCTTGGGGAAGCTTCTGCGAGAGAAACATATCTGCTTGGAG 358
QY 307 CTGTCGACCTTGAATGTTCTGCGACCTGACATGAGGTAGCGCTGAGACCTCTTATGGC 366
DB 359 CTGTCGACCTTGAATGTTCTGCGACCTGACATGAGGTAGCGCTGAGAGCTCTTATGGC 418
QY 367 CTGATGAGCCATGACAGGTATGCGGCAATTTGATCTCTGAAATTCATGACCTTCAT 426
DB 419 CTGATGAGCCATGACAGGTATGCGGCAATTTGATCTCTGAAATTCATGACCTTCAT 478
QY 427 GAGCCGAAAGATGCTGGATCATGATGATGATGATGATGATGATGATGATGATGATGATG 486
DB 479 GAGCCGAAAGATGCTGGATCATGATGATGATGATGATGATGATGATGATGATGATGATG 538
QY 487 TATAGACATACCATGATGACATGATGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 546
DB 539 CCTATATATATACCGGTATATACATGATGATGATGATGATGATGATGATGATGATGATG 598
QY 547 TCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 606
DB 599 TCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 658
QY 607 GCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 666
DB 659 GCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 718
QY 667 CTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726
DB 719 CTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 778
QY 727 AGCCCTTGTACCTGCTCTCTCCCACTGATTTGTGTGGGATGTTCTATGAGGCTGGAC 786
DB 779 AGCCCTTGTACCTGCTCTCTCCCACTGATTTGTGTGGGATGTTCTATGAGGCTGGAC 838
QY 787 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 846
DB 839 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 898
QY 847 TTTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
DB 899 TTTCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958
QY 907 GGTATGAGGAGGCTTGGAGGAGGCTCTGGGAAATTCATATGCTGGGCACTTTCCACGCT 966
DB 959 GGTATGAGGAGGCTTGGAGGAGGCTCTGGGAAATTCATATGCTGGGCACTTTCCACGCT 1018
  
```

QY 967 CTAGGAGAGA 977
 DB 1019 CTAGGAGAGA 1029

RESULT 4
 ADc85822
 ID ADc85822 standard; DNA; 1351 BP.

XX AC ADc85822;
 XX XX
 XX 01-JAN-2004 (first entry)
 XX XX
 DE Human GPCR gene SEQ ID NO:275.

KW ds; gene; human; GPCR;
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.

OS Homo sapiens.

XX EP1270724-A2.

XX 02-JAN-2003.

XX 18-JUN-2002; 2002EP-00013517.

XX 18-JUN-2001; 2001JP-00246789.

XX (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX

XX MPI; 2003-315783/31.
 XX P-PSDB; ADc85823.

PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.

XX Claim 1; SEQ ID NO 275; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADc85548-ADc87616 encode GPCR's of the
 CC invention.

XX Sequence 1351 BP; 342 A; 340 C; 295 G; 374 T; 0 U; 0 Other;

Query Match 85.5%; Score 835; DB 9; Length 1351;
 Best Local Similarity 91.2%; Pred. No. 5e-242;
 Matches 886; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

```

QY 7 AAAAAACACATCATGAGCTCCGAACTCCACTTTGGGAAAGCGCTTCATCTTGCGG 66
DB 188 AAGAAACACACGATGAGGCTCTGAACTTCACCTTGGAAGTGGCTTCATTTGGG 247
QY 67 GATTTGAATGACAGTGGGTCTCTGAACTGCTATGATGATTTACATTTACTATCAT 126
DB 248 GATTTGAATGACAGTGGGTCTCTGAACTGCTATGATGATTTACATTTACTATCAT 307
QY 127 GTTGGCACTGACGACGATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 186
DB 308 GTTGGCCCTGATGACGATGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367
QY 187 CATGCCATGATGATCTCTGCTGGGAGGCTCTCTCTCATGAGACCTCTGTTCAATCTGT 246
DB 368 CATGCCATGATGATCTCTGCTGGGAGGCTCTCTCTCATGAGACCTCTGTTCAATCTGT 427
  
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QY 247 TGTCACTCCCAAGGCTTGCGGAGCTTTCTGCGGAGAGAAAACATATCTCTTTGAGG 306
 DB 428 TGTCACTCCCAAGGCTTGCGGAGCTTTCTGCGGAGAGAAAACATCTCTTTGAGG 487
 QY 307 CTGTCACCTTGAGATGTTCTTGAGCACTGACATGGGTAGGAGGACCTCTACTAGG 366
 DB 488 CTGAGCCCTTGAGATGTTCTTGAGCACTGACATGGGTAGGAGGACCTCTACTAGG 547
 QY 367 CTTCATGCGCTTATGACAGATATGTTGCGGCACTTTGATCTCTGTAATACATGACCTCAT 426
 DB 548 CTTCATGCGCTTATGACAGATATGTTGCGGCACTTTGATCTCTGTAATACATGACCTCAT 607
 QY 427 GAGCCCAAGGCTTGCGGAGCTTTCTGCGGAGGCAATCTGATCTCTGATCTCTGATG 486
 DB 608 GAGCTCAAGGCTTGCGGAGCTTTCTGCGGAGGCAATCTGATCTCTGATCTCTGATG 667
 QY 487 TATAGACATATGACATGTTGAGCACTGACATGGGTAGGAGGACCTCTACTAGG 546
 DB 668 CTTAATATATACCTGTTGATGACATGCTCTCTGAGAGGCGGCAAGATCAGGCA 727
 QY 547 TCTGCTCTGAGATGCTGAGGCTTTGCTGAGGCTGCTGATGCTGATGCTGATG 606
 DB 728 TCTGCTCTGAGATGCTGAGGCTTTGCTGAGGCTGCTGATGCTGATGCTGATG 787
 QY 607 GCTTAAATATAGTACAGATGTTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
 DB 788 GCTTAAATATAGTACAGATGTTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 847
 QY 667 CTCTACACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
 DB 848 CTCTACACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907
 QY 727 AGCCCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 786
 DB 908 AGCCCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967
 QY 787 ATTCATGATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
 DB 968 ATTCATGATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1027
 QY 847 TTTCTACACATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
 DB 1028 TTTCTACACATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1087
 QY 907 GGTGATGCGGCTTTGAGAGGCTGCTGCGAATAATACATGCTGCTGCTGCTGCTGCTG 966
 DB 1088 GGTGATGCGGCTTTGAGAGGCTGCTGCGAATAATACATGCTGCTGCTGCTGCTGCTG 1147
 QY 967 CTAGGGAAGA 977
 DB 1148 CTAGGGAAGA 1158
 RESULT 5
 AAS11688
 ID AAS11688 standard; DNA; 1008 BP.
 AC AAS11688;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human odorant receptor (OR) DNA #5.
 XX
 XX Human; olfactory receptor; OR; G-protein coupled receptor superfamily;
 KW GPCR; gene therapy; triamniol; anti-HIV; cytoskeletal; ds;
 KW neotropic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;
 KW antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
 KW human immunodeficiency virus; neoplastic growth; neurological disorder;
 KW Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
 KW wound healing; asthma; Albinism; hereditary osteodystrophy;
 KW multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
 XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 27..1001
 FT /tag= a
 FT /product= "Human odorant receptor protein #5"
 PN W0200157215-A2.
 XX
 XX
 PD 09-AUG-2001.
 XX
 PF 07-FEB-2001; 2001WO-05003923.
 XX
 PR 07-FEB-2000; 2000US-0180511P.
 PR 07-FEB-2000; 2000US-0180630P.
 PR 07-FEB-2000; 2000US-0180646P.
 PR 08-FEB-2000; 2000US-0180930P.
 PR 08-FEB-2000; 2000US-0181004P.
 PR 08-FEB-2000; 2000US-0181013P.
 PR 08-FEB-2000; 2000US-0181043P.
 PR 24-JUL-2000; 2000US-0220262P.
 PR 25-JUL-2000; 2000US-0220594P.
 PR 11-AUG-2000; 2000US-0224596P.
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-00777789.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS;
 PI Baumgartner JC;
 DR WPI; 2001-488883/53.
 DR P-PSDB; AAU07088.
 XX
 PT Novel isolated NOX polypeptide related to human odorant receptor family
 PT of G-protein coupled receptor superfamily of proteins useful for treating
 PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
 XX
 PS Claim 9; Page 44; 199pp; English.
 XX
 CC Novel isolated NOX polynucleotides and their encoded polypeptides of the
 CC invention are related to the human olfactory (or odorant) receptors
 CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
 CC sequences are useful for treating or preventing a pathology associated
 CC with OR in a subject, and for manufacturing a medicament for treating a
 CC syndrome associated with a human disease. These diseases include
 CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
 CC growth, neurological disorders, such as Parkinson's disease and
 CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
 CC disease, multiple sclerosis, and Albinism hereditary osteodystrophy. The
 CC polynucleotides and polypeptides are also useful to identify proteins of
 CC the same family, to screen for molecules which inhibit or enhance the
 CC activity or function of olfactory receptors, to detect nasal epithelial
 CC neuronal tissue, in production of transgenic plants and for the
 CC development of new drug targets for various disorders. This sequence
 CC represents DNA encoding a human OR protein
 XX
 SQ Sequence 1008 BP; 216 A; 289 C; 234 G; 269 T; 0 U; 0 Other:
 Query Match 85.4%; Score 834; DB 5; Length 1008;
 Best Local Similarity 91.2%; Pred. No. 8.7e-242;
 Matches 885; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
 QY 8 AAAAAACATCATGAGAGCTCCGGAATCCACTTGGGAGAGGCTTCAATCTTGCGGAG 67
 DB 39 AACTCAACAGAGATGAGAGCTTGGAATCTCACTTGGGAGAGGCTTCAATCTTGCGGAG 98
 QY 68 ATTCTGAATGACAGAGGCTCTCTGAACTGCTCTATGCTGCTGCTGCTGCTGCTGCTG 127
 DB 99 ATTCTGAATGACAGAGGCTCTCTGAACTGCTCTATGCTGCTGCTGCTGCTGCTGCTG 158
 QY 128 TTGGCACTGACCAAGCAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 187

Db 159 TTGGCCCTGATGACGATGGGCTACTGCTCTGCTATATACGATGAGAGCCGGCTCCAC 218
 QY 188 ATGCCATGACTCTCTGCTGGGAGCTCTCTCATGAGACCTCTGTTCAATCTGTT 247
 Db 219 ATGCCATGACTCTCTGCTGGGAGCTCTCTCATGAGACCTCTGTTCAATCTGTT 278
 QY 248 GTCACTCCCAAGGCTTGGGAGCTTCTGCGGAGAGAAACATATCTCTTGGAGGC 307
 Db 279 GTCACTCCCAAGGCTTGGGAGCTTCTGCGGAGAGAAACATATCTCTTGGAGGC 338
 QY 308 TGTGACCTTCAAGTCTCTGCGGAGCTTCTGCGGAGAGAAACATATCTCTTGGAGGC 367
 Db 339 TGTGACCTTCAAGTCTCTGCGGAGCTTCTGCGGAGAGAAACATATCTCTTGGAGGC 398
 QY 368 TTTATGACCTTCAAGTCTCTGCGGAGCTTCTGCGGAGAGAAACATATCTCTTGGAGGC 427
 Db 399 TTTATGACCTTCAAGTCTCTGCGGAGCTTCTGCGGAGAGAAACATATCTCTTGGAGGC 458
 QY 428 AGCCCAAGGCTTGGGAGCTTCTGCGGAGAGAAACATATCTCTTGGAGGC 487
 Db 459 AGCCCAAGGCTTGGGAGCTTCTGCGGAGAGAAACATATCTCTTGGAGGC 518
 QY 488 ATAGACATACCATGATACATATGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 547
 Db 519 CTATATATACCGTATACATACATATGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 578
 QY 548 CTGCTCTGATGATCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
 Db 579 CTGCTCTGATGATCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 638
 QY 608 CTATATATACCGTATACATACATATGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 667
 Db 639 CTATATATACCGTATACATACATATGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 698
 QY 668 TCTACACACTAGTCTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
 Db 699 TCTATATACCAATTTACTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 758
 QY 728 GCGCTTGTACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
 Db 759 GCGCTTGTACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
 QY 788 TTTATGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847
 Db 819 TTTATGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
 QY 848 TTTATGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
 Db 879 TTTATGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938
 QY 908 GTCAATGCGGCTTGAAGAGGCTTCTGAGAAATATCATAGCTGCGCATTTCCACGCTC 967
 Db 939 GTCAATGCGGCTTGAAGAGGCTTCTGAGAAATATCATAGCTGCGCATTTCCACGCTC 998
 QY 968 TAGGAGAGA 977
 Db 999 TAGGAGAGA 1008

XX OS Unidentified.
 XX FH Location/Qualifiers
 FT Key 27.1001
 FT CDS /tag= a
 FT /product= "NOV6 protein"
 PN MO200236632-A2.
 PD 10-MAY-2002.
 PE 09-OCT-2001; 2001MO-US031744.
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-00777789.
 PR 20-SEP-2001; 2001US-00245292.
 XX (CURA-) CURAGEN CORP.
 PA Alsbrook JP, Burgess CE, Groesse WM, Lepley DW, Padigaru M,
 PI Spletter KA;
 DR WPI; 2002-471499/50.
 DR P-PSDB; AAU97927.
 XX New isolated olfactory receptor-like polypeptide, NOVX, useful for
 PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
 PT trauma, human immunodeficiency virus illness, neoplastic growth and
 PT neurological disorders.
 PS Claim 9; Page 33; 122pp; English.
 XX This invention relates to the DNA and protein sequences of a novel
 CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
 CC sequences of the invention and an antibody specific for the protein are
 CC useful for treating or preventing a disorder associated with NOV1 in a
 CC subject, preferably human. A NOVX specific antibody is useful for
 CC determining the presence or amount of protein in a sample. The DNA,
 CC protein and antibody of the invention is useful for diagnosing,
 CC preventing or treating disorders associated with aberrant NOVX expression
 CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
 CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
 CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
 CC antibody is useful in screening assays, detection assays (e.g.,
 CC chromosomal mapping, tissue typing, forensic biology), predictive
 CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
 CC trials and pharmacogenomic), and in methods of treatment (e.g.,
 CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
 CC produce antibodies immunospecific for the protein, to screen for
 CC potential agonist and antagonist compounds, and as bait protein in a two-
 CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
 CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
 CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
 CC invention is useful for isolating, and purifying the protein and to
 CC monitor protein levels in tissue as part of a clinical testing procedure.
 CC The present sequence represents the cDNA encoding the NOV6 protein of the
 CC invention
 XX Sequence 1008 BP; 216 A; 289 C; 234 G; 269 T; 0 U; 0 Other;
 QY Query Match 85.4%; Score 834; DB 6; Length 1008;
 Db Best Local Similarity 91.2%; Pred. No. 8.7e-242;
 Matches 885; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
 QY 8 AAAAAACATCATGAGAGCTCGGAATCCACTTGGGAGAGGCTCATCTTGGTGGG 67
 Db 39 AACTACCAAGCATGAGCTCTGGAATCTTCACTTGGGAGAGGCTCATCTTGGTGGG 98
 QY 68 ATTCTGAATGACAGTGGTCTCTGTAAGTCTGTAATTTAATCTTATCATG 127
 Db 99 ATTCTGAATGACAGTGGTCTCTGTAAGTCTGTAATTTAATCTTATCATG 158

RESULT 6
 ABK53096
 ID ABK53096 standard; cDNA; 1008 BP.
 XX AC ABK53096;
 XX DT 15-AUG-2002 (first entry)
 XX CDNA sequence encoding novel odourant receptor NOV6 protein.
 XX NOV; odourant receptor; G protein coupled receptor; GPCR; trauma; HIV;
 KM s8; gene; olfactory receptor; olfactory loss; neoplastic growth;
 KM human immunodeficiency virus; Alzheimer's disease; neurological disorder;
 KM Parkinson's disease.


```

QY 68 ATTCTGAATGACAGTGGGTCTCTGAACTGCTCTATGCTAATTATTAATCTTATACAG 127
DB 99 ATTCTGAATGACAGTGGGTCTCTGAACTGCTCTATGCTAATTATTAATCTTATACAG 158
QY 128 TTGGCACTGACGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
DB 159 TTGGCCCTGATGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 218
QY 188 ATGCCCATGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
DB 219 ATGCCCATGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 278
QY 248 GTCACTCTCCAAAGGCTTGGGAGGCTTCTGCGAGAGAGAGAGAGAGAGAGAGAGAG 307
DB 279 GTCACTCTCCAAAGGCTTGGGAGGCTTCTGCGAGAGAGAGAGAGAGAGAGAGAGAG 338
QY 308 TGTGCACTTGAAGTCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
DB 339 TGTGCACTTGAAGTCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 398
QY 368 TTCAATGCTTATGACAGGATATGAGGCAATTTGTCATCTCTGAAATCAATGACCTCATG 427
DB 399 TTCAATGCTTATGACAGGATATGAGGCAATTTGTCATCTCTGAAATCAATGACCTCATG 458
QY 428 AGCCCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
DB 459 AGCCCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 518
QY 488 ATAGACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 547
DB 519 ATAGACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578
QY 548 CTGCTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 607
DB 579 CTGCTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 638
QY 608 CTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
DB 639 CTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
QY 668 TCCATACACTAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 727
DB 699 TCCATACACTAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 758
QY 728 GCCCTGTGACCTGCTCTTCCACCTGATTTGTTGGTGGGATGTTTATGAGCTGCCACA 787
DB 759 GCCCTGTGACCTGCTCTTCCACCTGATTTGTTGGTGGGATGTTTATGAGCTGCCACA 818
QY 788 TTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847
DB 819 TTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
QY 848 TTCTACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
DB 879 TTCTACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938
QY 908 GTCAATGCGGGCTTGAAGAGGCTCTGCGAAATATCATATGCTGCGACATTTCCAGCTC 967
DB 939 GTCAATGCGGGCTTGAAGAGGCTCTGCGAAATATCATATGCTGCGACATTTCCAGCTC 998
QY 968 TAGGGAAGA 977
DB 999 TAGGGAAGA 1008

```

RESULT 8
AAS15914
AAS15914 standard; cDNA, 951 bp.

AC AAS15914;
XX
DT 25-JAN-2002 (first entry)

```

XX DNA encoding G-protein coupled receptor (GCRC) #18.
DE
XX G-protein coupled receptor; GCRC; vaccine; gene therapy;
XX cell proliferation disorder; cancer; arteriosclerosis;
XX neurodegenerative disorder; epilepsy; stroke; cardiovascular disorder;
XX hypertension; ischemic heart disease; gastrointestinal disorder;
XX anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
XX diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
XX schizophrenia disorder; neurodegenerative disorder; ss.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 1..951
XX FT /*tag= a
XX FT /product= "GCRC 18"
XX FT /note= "G-protein coupled receptor 18"
XX
XX MO20016742-A2.
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XX PD 13-SEP-2001.
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XX PF 01-MAR-2001; 2001MO-US006814.
XX
XX PR 03-MAR-2000; 2000US-0186854P.
XX PR 10-MAR-2000; 2000US-0188384P.
XX PR 17-MAR-2000; 2000US-0190453P.
XX PR 20-MAR-2000; 2000US-0190730P.
XX
XX (INCYTE GENOMICS INC.
XX
XX Lai P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CN;
XX Lu DM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J, Harland L;
XX Walsh RT, Lo TP, Borowsky ML;
XX
XX MPI; 2001-656776/75.
XX
XX DR P-PSDB; AAU10317.
XX
XX PT Novel G-protein coupled receptor polypeptides, for treating and
XX PT preventing autoimmune/inflammatory disorders, neurological disorders,
XX PT cell proliferative disorders, cardiovascular disorders and viral
XX PT infections.
XX
XX PS Claim 5; Page 139-140; 141pp; English.
XX
XX The invention describes a novel isolated polypeptide, selected from a
XX group of 21 G-protein coupled receptor polypeptides (GCRC) and useful in
XX vaccines and gene therapy. The polypeptide (I) is useful for screening
XX for agonist or antagonist of (I), compounds specifically binding to (I),
XX or compounds that modulate the activity of (I). The polynucleotide
XX encoding (I) is useful for screening a compound for effectiveness in
XX altering expression of a target polynucleotide comprising (II), by
XX exposing a sample comprising the target polynucleotide to a compound,
XX detecting altered expression of the target polynucleotide, and comparing
XX the expression of the target polynucleotide in the presence of varying
XX amounts of compound and in the absence of the compound. (I) and (II) are
XX useful for diagnosis, treatment and prevention of cell proliferative
XX disorders (e.g. cancer, arteriosclerosis, atherosclerosis), neurological
XX disorders (e.g. epilepsy, stroke, cardiovascular disorders (e.g. hypertension,
XX neurodegenerative disorder), gastrointestinal disorders (e.g. anorexia,
XX ischemic heart disease), autoimmune disorders (e.g. diabetes mellitus,
XX peptic ulcer), autoimmune/inflammatory disorders (e.g. inflammatory
XX osteoporosis, psoriasis), and metabolic disorders such as obesity.
XX Furthermore, the polynucleotide is useful as primers for detecting
XX single nucleotide polymorphisms; as elements in microarray, to monitor or
XX measure protein-protein interactions, drug-target interactions, and gene
XX expression profiles; to generate a transcript image of a tissue or cell
XX type, and to generate hybridisation probes useful in mapping the
XX naturally occurring genomic sequence. This sequence encodes G-protein
XX coupled receptor 18, one of 21 GCRC proteins described in the method of
XX the invention

```


Qy	200	CTCTCTGCTTGGGACACTCTCTCTCTCAATGGAACCCCGTTGACATCTGTGTCACTCCCAAG	259
Db	181	CTCTCTGCTTGGGACACTCTCTCTCAATGGAACCCCGTTGACATCTGTGTCACTCCCAAG	240
Qy	260	GCCTTGGCGGACTTCTCTGCGCAGAGAAAACTATCTCTCTTGGAGGCTGTGCATTGAG	319
Db	241	GCCCTTGGCGGACTTCTCTGCGCAGAGAAAACTATCTCTCTTGGAGGCTGTGCATTGAG	300
Qy	320	ATGTTCCTGGCACTGACAAATGGGATGCGCTGAGGACCTTCTACTGGCTTCATAGGCTAT	379
Db	301	ATGTTCCTGGCACTGACAAATGGGATGCGCTGAGGACCTTCTACTGGCTTCATAGGCTAT	360
Qy	380	GAAAGGTATGTGGCCATTGTCATCTCTGAAATATCATGACCCCTCATGAGCCCAAGATC	439
Db	361	GAAAGGTATGTGGCCATTGTCATCTCTGAAATATCATGACCCCTCATGAGCCCAAGATC	420
Qy	440	TGCTGTGATCATGGTGGCCACATCTGATCTCGGATCCCTGATTCCTATAGACATACC	499
Db	421	TGCTGTGATCATGGTGGCCACATCTGATCTCGGATCCCTGATTCCTATATATACC	480
Qy	500	ATGTACACTATGCACTCCCTTTCTGTGTGTCTCTGGAAATACAGGCACTGTGCTGTGAG	555
Db	481	GTGTATACCATATGCACTCCCTTTCTGTGTGTCTCTGGAAATACAGGCACTGTCTGTGAG	540
Qy	560	ATCCCAACCCCTGTGTAAGTTGGCCGTGTGTGATACCTCAAGGATGAGCTATATATAC	619
Db	541	ATCCCAACCCCTGTGTAAGTTGGCCGTGTGTGATACCTCAAGATGAGCTATATATAT	600
Qy	620	GTCACAGGTGTGACTTTCCTCTTGCTGCCCATTTTGTGCATTTGTGGCTCTTAACAATA	675
Db	601	GTCATGTGTGTGACTTTCCTCTTGCTGCCCATTTTGTGCATTTGTGGCTCTTAACAATA	660
Qy	680	GTCCTATTCATCTGTCTTGTGTGATGCAATAATGAGGGAGAGAAAGCCCTTGTCAAC	735
Db	661	ATTCTACTCACTGTGTGTGTGATGCAATAATGAGGGAGAGAAAGCCCTTGTCAAC	720
Qy	740	TGCTCTTCCCAACCTGATGTGTGTGGGATGTCTATGAGCTGCACATTCATGTATGTC	795
Db	721	TGCTCTTCCCAACCTGATGTGTGTGGGATGTCTATGAGCTGCACATTCATGTATGTC	780
Qy	800	TTGGCCAGTTCCTTCCACAGACCCCAACAAAGACATCATCTGTGTTTCTTACAAATT	855
Db	781	TTGGCCAGTTCCTTCCACAGACCCCAACAAAGACATCATCTGTGTTTCTTACAAATT	840
Qy	860	GTCACCTCAGCCCTGAAATTCATCTATACAGCTGAGAAATPAGAGGTCAATGCGGCC	911
Db	841	GTCACCTCAGCCCTGAAATTCATCTATACAGCTGAGAAATPAGAGGTCAATGCGGCC	900
Qy	920	TTGAGAGAGGTCTCTGGGAAATATCATCTGTGTGGCACTTCCACGCTCTAG	970
Db	901	TTGAGAGAGGTCTCTGGGAAATATCATCTGTGTGGCACTTCCACGCTCTAG	951
RESULT 10			
ABZ43126 standard; DNA, 951 BP.			
ABZ43126; ID			
ABZ43126; AC			
ABZ43126; XX			
06-MAR-2003 (first entry)			
Human GPCR polynucleotide SEQ ID NO 513.			
Human; GPCR; G protein coupled receptor; signal transduction; olfactory;			
drug development; gustatory; taste; fragrance; gene; ds.			
Homo sapiens.			
WO200216548-A2.			
28-FEB-2002.			
30-JUL-2001; 2001WO-IB001446.			

Query Match	Best Local Similarity	Matches	869; Conservative	0; Mismatches	82; Indels	0; Gaps	0;
XX 04-AUG-2000; 2000JP-00237818.							
PR 13-FEB-2001; 2001JP-00034434.							
XX (MISC-) JAPAN SCI & TECHNOLOGY CORP.							
PI Haga T, Takeda S, Mitaku S;							
XX WPI: 2002-304118/34.							
DR P-PSDB: ABP95852.							
XX Database global search for G protein-coupled receptors, proteins and							
PT encoded genes for studying in vivo signal transduction mechanism and							
PT identifying targets for drug development.							
XX Claim 9; SEQ ID NO 513; 97bp + Sequence Listing; Japanese.							
XX The invention relates to a method for screening G protein-coupled							
CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-							
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane							
CC domains with 250-1000 amino acid residues to give a gene homologous with							
CC a known GPCR gene. The receptor proteins and encoded genes are useful for							
CC studying in vivo signal transduction mechanism and identifying targets							
CC for drug development e.g. based on olfactory and gustatory receptors in							
CC form of agonists and antagonists by screening intrinsic and extrinsic							
CC ligands as bitter taste inhibitors, taste enhancers and fragrance							
CC improvers. Note: The sequence data for this patent did not form part of							
CC the printed specification, but was obtained in electronic format directly							
CC from WIPO at ftp.wipo.int/pub/published_pcr_sequences							
XX Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;							
XX							
83.9%; Score 819.8; DB 6; Length 951;							
91.4%; Pred. No. 1.7e-237;							
0; Mismatches 82; Indels 0; Gaps 0;							
20 ATGAGAGCTCGGGAAGCTCCACCTTTGGGAAAGCGGCTTCACTTGTGTGGGATTTCTGAATGAC 79							
1 ATGAGAGCTCGGGAAGCTCCACCTTTGGGAAAGTGGCTTCATTTGGTGGGAAATTCGAATGAC 60							
80 AGTGGGTCTCTCGGAACCTGCTCTAAGCTCAATTACAATCCATATGATGTGGCACTGAC 139							
61 AGTGGGTCTCTCGGAACCTGCTCTAAGCTCAATTACAATCCATATGATGTGGCACTGAC 120							
140 AGCAATGAGCTGCTGCTCCTGGGCATCAACATAGAAGCCGGCTCCACATGCCATGTAC 199							
121 AGCAATGAGCTGCTGCTCCTGGGCATCAACATAGAAGCCGGCTCCACATGCCATGTAC 180							
200 CTCCTGCTTGGGACAGCTCTCTCATATGAGACCTCTGTTCAATCTGTTGTCACTCCGAC 259							
181 CTCCTGCTTGGGACAGCTCTCTCATATGAGACCTCTGTTCAATCTGTTGTCACTCCGAC 240							
260 GCGTTGGCGGCACTTTCTGGGGAGAGAAAACAATATCTGTTGGAGGCGTGACACTTAC 319							
241 GCGCTTGGCGGCACTTTCTGGGGAGAGAAAACAATATCTGTTGGAGGCGTGACACTTAC 300							
320 ATGTTCTTGGCACTGACAAATGGGTGCTGTGAGGACCTTCTACTGGCTTCAATGGGCTAT 379							
301 ATGTTCTTGGCACTGACAAATGGGTGCTGTGAGGACCTTCTACTGGCTTCAATGGGCTAT 360							
380 GACAGGTATGTGGCCATTGTCATCTCTGAATATGACCTCTATGAGCCCAAGATC 439							
361 GACAGGTATGTGGCCATTGTCATCTCTGAATATGACCTCTATGAGCCCAAGATC 420							
440 TGTGATCATGTGGCCACATCTCGGAATCTGGGATCTCCCTATATGCTADAGACATACC 499							
421 TGTGATCATGTGGCCACATCTCGGAATCTGGGATCTCCCTATATGCTADAGACATACC 480							
500 ATGTACATATGACCTCCCTTCTGTGTGCTCTGGGAAATCAGGACATCTGCTGTGAG 559							
481 GTGTATACATATGACCTCCCTTCTGTGTGCTCTGGGAGGCCAGAGATCAGGATCTTCTGTGAG 540							
560 ATGCCACCTTGTGGAAGTTGGCTGTGCTGATTAACCTCAGGTATGAGCTTATATATATAC 619							

Db 541 ATCCACACTTGTGAGAGTGGCTGTGCTGATACCTCCAGATATGAGCTATGTTAT 600
Qy 620 GTGACAGGTGATCTTTCTCTGTGCTCCCATTTTGTGCAATTTGGCTCTTACACTA 679
Db 601 GTGATGGGTGATCTTCTGATTCCTCTCTGTGCTGATATGAGCTCTCTATACAA 660
Qy 680 GTCCATATCATCTGTGCTTGTATGCAATCAATAGAGGAGAGAAAGCCCTGTAC 739
Db 661 ATTCTACATCATCTGTGCTTCAATATGCAATCAATAGAGGAGAGAAAGCCCTGTAC 720
Qy 740 TGCTCTTCCACCTGATTTGTGCTGGATGTTCTATGAGAGTGTGCAATCATGATATG 799
Db 721 TGCTCTTCCACCTGATTTGTGCTGGATGTTCTATGAGAGTGTGCAATCATGATATG 780
Qy 800 TTGGCCAGTCTTCTTCCACAGGCCCAAGACAAATCATCTGTGTTTCTACAAAT 859
Db 781 TTGGCCAGTCTTCTTCCACAGGCCCAAGACAAATCATCTGTGTTTCTACAAAT 840
Qy 860 GTCACTCCAGCCCTGATTCATCATCTATGAGAGTGTGCAATGAGAGTGTATGCGGCC 919
Db 841 GTCACTCCAGCCCTGATTCATCATCTATGAGAGTGTGCAATGAGAGTGTATGCGGCC 900
Qy 920 TTGAGAGAGGTCTCTGGGAAATATCATCTGCTGGACATTCACGCTCTAG 970
Db 901 TTGAGAGAGGTCTCTGGGAAATATCATCTGCTGGACATTCACGCTCTAG 951

RESULT 11

ABK68461
ID ABK68461 standard; DNA; 951 BP.

XX AC ABK68461;

XX DT 02-JUL-2002 (first entry)

XX DE Human DNA for olfactory and pheromone G protein-coupled receptor #61.

XX KM Human; ds; gene: olfactory and pheromone G protein coupled receptor;
XX KM GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
XX KM anorectic; taste; fragrance; food additive; cosmetic; cell migration;
XX KM sterility; psychotic disorder; neurological disorder; anxiety;
XX KM schizophrenia; manic depression; depression; axonal growth;
XX KM menstrual cycle; appetite sexual motivation; sexual attraction;
XX KM aggression.

XX OS Homo sapiens.

XX PN WO200224726-A2.

XX PD 28-MAR-2002.

XX PF 21-SEP-2001; 2001WO-BE000162.

XX PR 22-SEP-2000; 2000EP-00870211.

XX PA (CHEM-) CHEMCOM SA.

XX PI Veichen A;

XX DR MPI, 2002-330013/36.

XX DR P-PSDB; AAU95574.

XX PT Novel pheromone G-protein coupled receptor and receptor-derived agonists,
XX PT antagonists or inhibitors useful in food or cosmetic products or in the
XX PT treatment or prevention of neurological disorders such as anxiety and
XX PT schizophrenia.

XX PS Disclosure; Page 196-197; 833BP; English.

XX CC The invention relates to olfactory and Pheromone G-protein coupled
XX CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
XX CC portion and its encoding polynucleotide. Also included are an agonist,

CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector
CC comprising the polynucleotide, a cell transformed by the vector, a non-
CC human mammal comprising a partial or total deletion of the polynucleotide
CC encoding the receptor and screening (detection and possibly, recovering)
CC of compounds which are known or not known to be agonist, antagonists or
CC inhibitors of natural compounds to the GPCR. The receptor-derived
CC agonists, antagonists, inhibitors or compounds are used as an
CC improvement, elimination or substitution of an existing taste and/or a
CC fragrance of (or in) the food and/or cosmetic products. They can also be
CC used in the preparation of medicament in the treatment and/or prevention
CC of a mammalian disorder, such as cell migration, sterility, psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, depression, for promoting axonal growth, nerve cell
CC connection and nerve regeneration for modulating male and female
CC endocrine functions, hormone production and the menstrual cycle, for the
CC prevention or the treatment by stimulation of several mammalian
CC behaviours, such as stimulation or suppression of appetite, sexual
CC motivation, sexual attraction, aggression and for promoting or
CC suppressing chemical communication between organisms. The present
CC sequence is a human DNA encoding an olfactory and pheromone GPCR
XX

SQ Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

Query Match 83.3%; Score 819.8; DB 6; Length 951;
Best Local Similarity 91.4%; Pred. No. 1.7e-237;
Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 20 ATGAGATCCGGAACCTCCAGCTTGGGAGAGGCGGCTTATCTTGGTGGGATTTGATGAC 79
Db 1 ATGAGAGCTCTGGAACTTCACTTGGGAGAGGCGGCTTATCTTGGTGGGATTTGATGAC 60
Qy 80 AGTGGGTCTCTGAACTGCTCTATGTAACATTACATCTTATGATGAGGAGTACC 139
Db 61 AGTGGGTCTCTGAACTGCTCTATGTAACATTACATCTTATGATGAGGAGTACC 120
Qy 140 AGCAATGCTGTGCTCTCTCTGACATACCATAGAAAGCGGCTCCACATGCCATGTAC 199
Db 121 AGCAATGCTGTGCTCTCTCTGACATACCATAGAAAGCGGCTCCACATGCCATGTAC 180
Qy 200 CTCCTGCTTGGGAGAGCTCTCTGACATGAGACCTCTCTGATCATCTGTGATCTCCAG 259
Db 181 CTCCTGCTTGGGAGAGCTCTCTGACATGAGACCTCTCTGATCATCTGTGATCTCCAG 240
Qy 260 GCGTTGGCGAGCTTCTGCGAGAGAAACATATCTCTCTTGGAGAGTGTGACCTGAG 319
Db 241 GCGTTGGCGAGCTTCTGCGAGAGAAACATATCTCTCTTGGAGAGTGTGACCTGAG 300
Qy 320 ATGTTCTTGGCACTGACAAATGAGAGCGCTGAGACCTCTTACCTGATGAGGCTAT 379
Db 301 ATGTTCTTGGCACTGACAAATGAGAGCGCTGAGACCTCTTACCTGATGAGGCTAT 360
Qy 380 GACAGGATGAGGCACTTGTGATCTCTGAAATATACATACCTCTATGAGCCCAAGATC 439
Db 361 GACAGGATGAGGCACTTGTGATCTCTGAAATATACATACCTCTATGAGCCCAAGATC 420
Qy 440 TGCTGATCATGAGTGGCAATCTGATCTCTGAGATCCCTGATAGAGGATCTTCTGTGAG 499
Db 421 TGCTGATCATGAGTGGCAATCTGATCTCTGAGATCCCTGATAGAGGATCTTCTGTGAG 480
Qy 500 ATGTACATATGACCTCTCTTGTGTGTGCTTGGGAAATGAGGATCTGCTGTGAG 559
Db 481 ATGTACATATGACCTCTCTTGTGTGTGCTTGGGAAATGAGGATCTTCTGTGAG 540
Qy 560 ATCCAGCCTTGTGAAATGAGTGGCGGTGTGATCTCTGAGTATGAGTATATATATG 619
Db 541 ATCCAGCCTTGTGAAATGAGTGGCGGTGTGATCTCTGAGTATGAGTATATATATG 600
Qy 620 GTGACAGGTGATCTTCTCTTGTGCTCCCATTTTGCATATGAGGCGCTTACACATA 679
Db 601 GTGATGGGTGATCTTCTCTTGTGCTCCCATTTTGCATATGAGGCGCTTACACATA 660
Qy 680 GTCCATATCATCTGTGCTTGTATGCAATCAATAGAGGAGAGAAAGCCCTGTAC 739

Db 661 ATTCTACTGACTGTGCTCCATATGTCATCAATGAGGGAGGAGAAAGCCCTTGTACCC 720
 QY 740 TGGCTTTCCCACTGATTTGGTGGGAGTGTCTTAAGAGCTCCCACTTCATGTAATGTC 799
 Db 721 TGGCTTTCCCACTGATTTGGTGGGAGTGTCTTAAGAGCTCCCACTTCATGTAATGTC 780
 QY 800 TTGCCCAGTTCTTCCACAGAGCCCAACAGACATCATCTCTGTTTTCTACACAAAT 859
 Db 781 TTGCCCAGTTCTTCCACAGAGCCCAACAGACATCATCTCTGTTTTCTACACAAAT 840
 QY 860 GTCACTCCAGCCCTGAAATCCATCTATCTACAGCTTGAAGAAATGAAGATGCGGACC 919
 Db 841 GTCACTCCAGCCCTGAAATCCATCTATCTACAGCTTGAAGAAATGAAGATGCGGACC 900
 QY 920 TTGAGAGAGGCTCTGGGAAAATATATCTGCTGGCAATTCAGGCTCTAG 970
 Db 901 TTGAGAGAGGCTCTGGGAAAATATATCTGCTGGCAATTCAGGCTCTAG 951

RESULT 12

ABK37593
 ID ABK37593 standard; cDNA; 951 BP.

XX ABK37593;

XX 08-MAY-2002 (first entry)

XX DNA encoding G-coupled olfactory receptor #95.

XX Human; olfactory G-coupled receptor; sensory perception of odourant;
 XX odour composition; taste composition; gene; ss.

XX Homo sapiens.

XX MO200198526-A2.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US020122.

XX 22-JUN-2000; 2000US-0213812P.

XX 13-MAR-2001; 2001US-00804291.

XX (SENO-) SENOMX INC.

XX Zozulya S, Stryer L;

XX WPI; 2002-083330/11.

XX P-PSDB; AAU85234.

XX Representing sensory perception of one or more odourants for the
 XX identification and design of tastes and odors comprises providing a
 XX representative group of n olfactory receptors.

XX Example; Page 101; 182pp; English.

XX The invention relates to a method of representing sensory perception of
 XX one or more odourants. The method comprises: (a) providing a
 XX representative class of n olfactory receptors or ligand binding domains
 XX (LBD) of these receptors; (b) measuring values X1 to Xn representative of
 XX at least one activity of one or more odourants selected from: (i) binding
 XX one or more odourants to the LBD of at least one of the n olfactory
 XX receptors; (ii) activating at least one of the n olfactory receptors with
 XX the one or more odourants; and (iii) blocking at least one of the n
 XX olfactory receptors with the one or more odourants; and (c) generating a
 XX representation of sensory perception from the values X1 to Xn. The
 XX representation of the sensory perception of odourants is useful for the
 XX design and formulation of odour and taste compositions. ABK37499-ABK37754
 XX and ABK37918-ABK37921 represent human olfactory G-coupled receptor coding
 XX sequences and related PCR primers of the invention

SQ Sequence 951 BP; 199 A; 275 C; 218 G; 259 T; 0 U; 0 Other;

Query Match 83.9%; Score 819.8; DB 6; Length 951;
 Best Local Similarity 91.4%; Pred. No. 1.7e-237;
 Matches 869; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 20 ATGAGAGCTCCGAAACATCCACCTTGGGAGCGCTTCATCTGGTGGGAGATTCTGAATGAC 79
 Db 1 ATGAGAGCTCCGAAACATCCACCTTGGGAGCGCTTCATCTGGTGGGAGATTCTGAATGAC 60
 QY 80 AGTGGGTCTCTGAACTGCTCTATAGCTATTTACATTCCTATATCATGTTGGACCTGACC 139
 Db 61 AGTGGGTCTCTGAACTGCTCTATAGCTATTTACATTCCTATATCATGTTGGACCTGACC 120
 QY 140 AGCAATGATGCTGCTCTCTGCTGACATCACCATTGAAGCCCGGTCCACATGCCCATGAC 129
 Db 121 AGCAATGATGCTGCTCTCTGCTGACATCACCATTGAAGCCCGGTCCACATGCCCATGAC 180
 QY 200 CTCCTGTTGGGAGAGCTCTCTCATGAGACCTCTGTTCACATCTGTTGCTCACTCCCAAG 259
 Db 181 CTCCTGTTGGGAGAGCTCTCTCATGAGACCTCTGTTCACATCTGTTGCTCACTCCCAAG 240
 QY 260 GCCTTGGCGGACTTTCTGCGCAGAGAAAACATATCTCTTTGGAGGCTGTGACTTACG 319
 Db 241 GCCTTGGCGGACTTTCTGCGCAGAGAAAACATATCTCTTTGGAGGCTGTGACTTACG 300
 QY 320 ATGTTCTTGGCACTGACAAATGGGTAGGCTGAGAGACCTCTACTGCTTCATGAGCCTAT 379
 Db 301 ATGTTCTTGGCACTGACAAATGGGTAGGCTGAGAGACCTCTACTGCTTCATGAGCCTAT 360
 QY 380 GACAGGATGATGGGCATTTGTCTATCTCTGAAATATACATGAGCCCTCATGAGCCCAAGAGTC 439
 Db 361 GACAGGATGATGGGCATTTGTCTATCTCTGAAATATACATGAGCCCTCATGAGCCCAAGAGTC 420
 QY 440 TGGTGATCATGATGAGCCACATCTGATCTGAGATCTGATCTGATCTGATCTGATCTGAT 499
 Db 421 TGGTGATCATGATGAGCCACATCTGATCTGAGATCTGATCTGATCTGATCTGATCTGAT 480
 QY 500 ATGATACATATGACCTCCCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 559
 Db 481 ATGATACATATGACCTCCCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 540
 QY 560 ATCCACCTTGGCTGAGAGTTGGCTGTGATGATCTGATGATGATGATGATGATGATGATGAT 619
 Db 541 ATCCACCTTGGCTGAGAGTTGGCTGTGATGATCTGATGATGATGATGATGATGATGATGAT 600
 QY 620 GTGAAGGTGATGATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679
 Db 601 GTGAAGGTGATGATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 680 GTCTATTCATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 739
 Db 661 ATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 740 TGGCTTTCCCACTGATTTGGTGGGAGTGTCTTAAGAGCTCCCACTTCATGTAATGTC 799
 Db 721 TGGCTTTCCCACTGATTTGGTGGGAGTGTCTTAAGAGCTCCCACTTCATGTAATGTC 780
 QY 800 TTGCCCAGTTCTTCCACAGAGCCCAACAGACATCATCTCTGTTTTCTACACAAAT 859
 Db 781 TTGCCCAGTTCTTCCACAGAGCCCAACAGACATCATCTCTGTTTTCTACACAAAT 840
 QY 860 GTCACTCCAGCCCTGAAATCCATCTATCTACAGCTTGAAGAAATGAAGATGCGGACC 919
 Db 841 GTCACTCCAGCCCTGAAATCCATCTATCTACAGCTTGAAGAAATGAAGATGCGGACC 900
 QY 920 TTGAGAGAGGCTCTGGGAAAATATATCTGCTGGCAATTCAGGCTCTAG 970
 Db 901 TTGAGAGAGGCTCTGGGAAAATATATCTGCTGGCAATTCAGGCTCTAG 951

RESULT 13

AAH31854
 ID AAH31854 standard; DNA; 948 BP.

XX

PR	07-SEP-2000; 2000US-0230732P.	
PR	07-FEB-2001; 2001US-0266862P.	
XX		
PA	(SENO-) SENOMYX INC.	
XX		
P1	Zozulya S;	
XX		
DR	WPI; 2001-570867/64.	
XX	P-PSDB; AAU24730.	
PT	Nucleic acids encoding human olfactory G protein-coupled receptors.	
PT	Useful for screening for compounds involved in olfactory sensation, where	
PT	the compounds can be used in the food, pharmaceutical and cosmetic	
PT	industries to customize odors.	
XX		
P5	Claim 1; Page 180; 319pp; English.	
CC	The invention relates to nucleic acids encoding human olfactory	
CC	receptors, OR, (a G protein-coupled receptor, GPCR). The OR's	
CC	specifically recognise molecules, odorants, that elicit specific	
CC	olfactory sensation. The human olfactory receptors and polynucleotides	
CC	encoding them are useful for screening a library of chemical compounds	
CC	for compounds that are involved in olfactory sensation. Modulators of	
CC	their activity are useful for pharmacological and genetic modulation of	
CC	olfactory signalling pathways. Therefore, they can be used in the food,	
CC	pharmaceutical and cosmetic industries to customise odours and	
CC	fragrances. The present sequence encodes a human olfactory receptor of	
CC	the invention	
XX		
SQ	Sequence 975 BP; 189 A; 299 C; 217 G; 270 T; 0 U; 0 Other;	
Query Match	34.6%; Score 338; DB 5; Length 975;	
Best Local Similarity	61.2%; Pred. No. 1.5e-91;	
Matches 545; Conservative	0; Mismatches 345; Indels 0; Gaps 0	
QY	52 CTTCACTCTGGGGGATTCGAATGACAGTGGGATCTCTCGTAACCTGCTATGCTACATT	111
DB	36 CTTGCTCCTCAAGGCGCTCATGCCATCTGCTGCTTCCCGGGCTTCTCTTGGAATAGT	95
QY	112 TACAACTCTAATACATGTTGGCACTGCACGACGAATGATCTGCTGCTCTTGCCATACCAAT	171
DB	96 CTTCTCCATCTTGTGTGGTGGCTATAACACGCAACCTTGTCATGATTTCTCTATCCACAT	155
QY	172 AGAAGCCGGGCTCCACATGCCCATGACCTCTGCTTGGGGAGCTCTCTCATGACCT	231
DB	156 GGAATCCGCGCTCCACACACCATGATCTTTGCTCAAGCAGCTCTCCATATGATGATAC	215
QY	232 CCGTTTCACATCTGTTGTCACTCCCAAGGCTTTGGCGGACTTTTCGGGAGAGAAACAC	291
DB	216 CATCTACATCTGATACATGTCCTCCCAAGATGCTCCAGACCTCTGCTCCAGACAAAGAC	275
QY	292 TATTCCTCTTGGAGGCGTGGACCTTGAGATGTTCCAGCACTGACGAATGAGATGGAGCTGA	351
DB	276 CATTTCTTCTCGGGGCTGTGGCAATTAAGATCTTCTCTTACTTGAACCTGATTTGGAAGGGA	335
QY	352 GGACCTCTCACTGCGCTTATGAGCTGACATGACAGATATGAGCCATTGTCATCTGTGAA	411
DB	336 ATTTCTTCTCGTGGGCTCATGAGCTATGACCGCTATGAGGCTGTGTGCAACCTCTACG	395
QY	412 ATTCATGACCTCTATGAGCCCAAGAGTCTGCTGGAATCATGATGTGGCAATCTCGATGCTCT	471
DB	396 GTACCTCTCTCTATGAACCGAGGGGTGCTTAATTCATGATGATGGGCTCTCGGGGTGG	455
QY	472 GGATCCCTGATGTGCTATAGACATATACATGATCACTATCACTCCCTTCTGTGTGTC	531
DB	456 TGTGTTCTTGGATGGGTTATGCTGATCTCTGTACATATGATTTCCCTTCTGTGATC	515
QY	532 CTGGGAATCAAGGCATCTGCTCTGTGAGATCCACCTTGTCTGAAGTGGCTGTGCTGA	591
DB	516 CCGAGAGATCAATCATCTTTTCTGTGAGATCCGAGCCGTGCTGAAGTGTCTTGACAGA	575
QY	592 TACCTCAGGTATGAGCTTATATATACGTGACAGGTGACATTTCTCTTGGCTCCCAT	651

Db	576	CAAGTCACTCTAATGAGAACCCGTGATGTATGCTGATGCTGATTCCTCT	635
Qy	652	TTCTGCCATTGTGCGCTCTCTACACACTGATTCCTATTCACCTGTGTTGGTATGCCATGAAA	711
Db	636	ATCTGTATCTCTGTCTCTCCACACAGCAATCTCTGACCTGTCCACAGATGAACTCTGC	695
Qy	712	TGAGGGGAGGAAAGAACCCCTTGTACCTGCTCTTCCGCACTGATTTGGTCGGGATGTT	771
Db	696	TGAGGGCCGGGCGCAAGGCTTTTGTCTACGTGTCTCTCCACATTTATGGTGGTGAGCGTTT	755
Qy	772	CTATGAGCTGCCACATTCATGTATGTCTTGGCCAGTTCCTTCCACAGCCCCAAACAGA	831
Db	756	CTACGGGGCAGCGCTTCTACACCAACAGTGCGCCCCCACTCTACACACTCCAGAGAAA	815
Qy	832	CAACATCATCTCTGTGTTTCTTACACAAATTTGTACTCCAGCCTGAAATCCACTCATCTCAG	891
Db	816	TAAAGTGTGTCTCTCCCTTCTACACACTCTCACCCCACTGTCTAACCCACTCATCTACAG	875
Qy	892	CCTGAGGAATTAAGGAGGTCATGCGGGCCCTGAGGAGGATCTCTGGAAAAAT	941
Db	876	CTTAGGATTAAGATGTGTGCTGCAAGCTCTGAGGAAAGTACTTAGGAGAT	925
RESULT 15			
ABZ43145			
ID	ABZ43145	standard; DNA; 975 BP.	
XX	ABZ43145;		
AC			
XX			
DT	06-MAR-2003	(first entry)	
XX			
DE	Human GPCR polynucleotide SEQ ID NO 551.		
XX			
KW	Human; GPCR; G protein coupled receptor; signal transduction; olfactory;		
XX	drug development; gustatory; taste; fragrance; gene; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200216548-A2.		
XX			
PD	28-FEB-2002.		
XX			
PF	30-JUL-2001; 2001WO-IB001446.		
XX			
PR	04-AUG-2000; 2000JP-00237818.		
XX			
PR	13-FEB-2001; 2001JP-00034434.		
XX			
PA	(NISC-) JAPAN SCI & TECHNOLOGY CORP.		
XX			
PI	Haga T, Takeda S, Mitaku S;		
XX			
DR	WPI; 2002-304118/34.		
XX			
DR	P-PsDB; ABP95871.		
PT			
XX			
PT	Database global search for G protein-coupled receptors, proteins and		
XX	encoded genes for studying in vivo signal transduction mechanism and		
XX	identifying targets for drug development.		
XX			
PS	Claim 9; SEQ ID NO 551; 97bp + Sequence Listing; Japanese.		
XX			
CC	The invention relates to a method for screening G protein-coupled		
CC	receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-		
CC	ABP95942) by extracting open-reading frames containing 6-8 transmembrane		
CC	domains with 250-1000 amino acid residues to give a gene homologous with		
CC	a known GPCR gene. The receptor proteins and encoded genes are useful for		
CC	studying in vivo signal transduction mechanism and identifying targets		
CC	for drug development e.g. based on olfactory and gustatory receptors in		
CC	form of agonists and antagonists by screening intrinsic and extrinsic		
CC	ligands as bitter taste inhibitors, taste enhancers and fragrance		
CC	improvers. Note: The sequence data for this patent did not form part of		
CC	the printed specification, but was obtained in electronic format directly		
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences		
XX			

SQ Sequence 975 BP; 189 A; 299 C; 217 G; 270 T; 0 U; 0 Other;

Query Match 34.6%; Score 338; DB 6; Length 975;

Best Local Similarity 61.2%; Pred. No. 1.5e-91;

Matches 545; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

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REFERENCE		3 Shihata,K., Itoh,M., Aizawa,K., Nagoaka,S., Sasaki,N., Carninci,P., Komono,H., Akiyama,U., Niishi,K., Kitsuana,T., Tashtiro,H., Itoch,M., Sumi.N., Ishii,Y., Nakamura,S., Hazama.M., Ninshin.T., Harada,A., Yamamoto,R., Matsumoto.H., Sakaguchi.S., Ikegami.T., Kasaihiagi.K., Fujiwaki,S., Inoue,K., Togawa.Y., Izawa.M., Ohara.E., Watabiki.M., Yoneda.Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsumura,S., Kawai,J., Okazaki,Y., Muramatsu.M., Inoue,Y., Kirz.A. and Hayashizaki.Y.
JOURNAL MEDLINE PUBLISHED REFERENCE		Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
AUTHORS		4
TITLE		The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
JOURNAL		Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
AUTHORS		5
TITLE		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
JOURNAL		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cdnas Nature 420, 563-573 (2002)
REFERENCE		Nature 420, 563-573 (2002) 6 (bases 1 to 1394)
AUTHORS		Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Atakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukushima,Y., Furuno,M., Hanagaki,T., Hara,A., Hayasato,N., Hiramoto,K., Hisataka,T., Horl,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kitayama,T., Kato,H., Kawai.J., Koijima.Y., Konno.H., Kouda.M., Koya,S., Kuithara,C., Matsuura.T., Miyazaki.A., Nishii,K., Nomura,K., Numazaki.R., Ono,M., Okazaki,Y., Okido,T., Owa.C., Saito,H., Satto,R., Sakai,C., Sakai,K., Sano.H., Sasaki,D., Shibata,K., Shihata,Y., Shinigawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami.M., Tagawa.A., Takahashi.F., Tanaka,T., Tejima.Y., Toya.T., Yamamura.T., Yasunishi.A., Yoshida.K., Yoshiro.M., Muramatsu.M. and Hayashizaki,Y.
TITLE		Direct Submission
JOURNAL		Submitted (10-JUL-2000) Yoshitake Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail:genome-res@gsc.riken.go.jp, url:http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/ , Tel:81-45-503-9222, Fax:81-45-503-9216]
COMMENT		Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GGAAGAGAAGATCCCAAGACCTGTATTTCCTTTTTCATA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence 15' GGAGCAGCATTCGCAGTAATTAATTAATNCCCCCCC 3'. cDNA was cleaved with BamI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified plusscript KS(+) after bulk excision from Lambda PLC I. Cloning sites, 5' end: SalI, 3' end: BamHI. Host: DHIOB. Location/Qualifiers 1..1394 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" / db_xref="PMID:4933433E02" / db_xref="PANTOM_DB:4933433E02" / db_xref="MGI:1894709" / db_xref="taxon:10090" /clone_id="4933433E02" /sex="male" /tissue_type="testis" /clone_lib="RIKEN full-length enriched mouse cDNA library"

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ACCESSION	AK016560		
VERSION	AK016560.1	GI:12855357	
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SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	6 (bases 1 to 3063)		
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirooka, T., Horii, F., Imclani, K., Ishii, Y., Itoh, M., Iwawa, M.,		

TITLE
JOURNAL

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
Riken Yokohama Institute, E-1-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222,
Fax:81-45-503-9216)

Direct Submission

Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

for further details

please visit our web site (<http://genome.gsc.riken.go.jp/>)

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FEATURES
    source
        1..3063
            Location/Qualifiers
                cDNA library was prepared and sequenced in Mouse Genome
                Encyclopedia project of Genome Exploration Research Group in Riken
                Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                Division of Experimental Animal Research in Riken contributed to
                prepare mouse tissues. First strand cDNA was primed with a primer
                [5' GAGAGAGGAGGAGATCCAAAGACTCTTTTTTTTTTTTTTAA 3'], cDNA was
                prepared by using trehalose thermo-activated reverse transcriptase
                and subsequently enriched for full-length by cap-trapper. Second
                strand cDNA was prepared with the primer adapter of sequence [5'
                GAGAGGAGATCTCCAGTTATTAATATTAATCCCCCCCCCCC 3']. cDNA was cleaved
                with BamHI and XhoI. cDNA of size comprised longer than 7 kb was
                selected before cloning. Vector: a modified plasmidscript KS(+) after
                bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
                end: BamHI. Host: DH10B.
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ORIGIN

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KEYWORDS GSS,
SOURCE Pan troglodytes (chimpanzee)

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ORGANISM Pan troglodytes
REFERENCE Bukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
TITLE 1
JOURNAL Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
AUTHORS Totoki, Y., Watanabe, H., and Sakaki, Y.
REFERENCE BAC end sequences of library PTB
AUTHORS Unpublished
TITLE 2 (bases 1 to 710)
JOURNAL Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
AUTHORS Totoki, Y., Watanabe, H., and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
AUTHORS and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
TITLE 1-7-22 Suehiro-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
JOURNAL (E-mail: chimpanzee@sc.riken.go.jp, URL: http://hsp.sec.riken.go.jp/,
AUTHORS Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end
PRIMERS was generated during the R&D process and may have higher chance of
clone tracking errors.
Sequencing: -21M13
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Vector : pKS145
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Best Local Similarity 97.6%; Pred. No. 1,3e-161;
Matches 616; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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Db 75 GAGATCCGGAATCCACCTTGGGAAAGCGGCTTCACTTGTGGGAGATTCTGAATGACAG 134
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ACCESSION AG090554
VERSION AG090554.1 GI:16642356
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
TITLE Tokoki, Y., Watanabe, H. and Sakaki, Y.
JOURNAL BAC end sequences of library PTB
REFERENCE 1
2 (bases 1 to 663)
Unpublished
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Tokoki, Y., Watanabe, H. and Sakaki, Y.
DIRECT SUBMISSION
Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Shohiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
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Best Local Similarity 91.2%; Pred. No. 9.9e-136;
Matches 548; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 23 GAGCTCGGAACCTCCAGCTTGGAGGCGCTTACTTGTGGGATTTGTAATGACAGT 82
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QY 83 GGGTCTCTGAACGCTCTATGCTACATTTACATCTTATACATGTTGGACCTGACACGC 142
DB 121 GGGTCTCTGAACGCTCTATGCTACATTTACATCTTATACATGTTGGACCTGACACGC 180
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QY 383 AGTATGTGGCCATTTGTCTCTCTGAAATATACATGACCTCATGAGCCCAAGGCTTGC 442
DB 421 AGTATGTGGCCATTTGTCTCTCTGAAATATACATGACCTCATGAGCCCAAGGCTTGC 480
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DB 661 A 661

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DEFINITION IM0125N08F Mouse 10kb plasmid UUC1M library Mus musculus genomic
ACCESSION AZ373068
VERSION AZ373068.1 GI:10486768
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
TITLE Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT Contact: Robert B. Weiss
UNIVERSITY University of Utah
ADDRESS Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
TEL: 801 585 5606
FAX: 801 585 7177
EMAIL: ddunn@genetics.utah.edu
INSTRUMENT Insert Length: 10000 Std Error: 0.00
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CLASS: plasmid ends
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ORIGIN
 Query Match 41.9%; Score 409.2; DB 28; Length 625;
 Best Local Similarity 78.6%; Pred. No. 3.2e-105;
 Matches 489; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

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Qy  GTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
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RESULT 6 BY16264 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

BY16264 968 bp mRNA linear EST 17-DEC-2002
 BY16264 RIKEN full-length enriched, adult male testis Mus musculus
 cDNA clone 493244H21 5', mRNA sequence.
 BY16264.1 GI:27129381
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 968)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nishida, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
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 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
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 Wells, C., Wilming, L.G., Wyszewski, B., Yanagisawa, M., Yang, I.,
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 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 12466851
 22354683
 CONTACT: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Saito-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Horii, F.,
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 Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watanabe, K., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multichannel sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source

Location/Qualifiers
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 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GAGAGGAGAGGCGCGCAATTATTTCTCAGTTAATTAATTCCTCCCCCCC
 3']. cDNA was cloned into the XhoI and BamHI sites."

ORIGIN

Query Match 33.2%; Score 324; DB 13; Length 968;
 Best Local Similarity 79.6%; Pred. No. 8.5e-81;
 Matches 395; Conservative 0; Mismatches 100; Indels 1; Gaps 1;
 1 GCACTTAAACACATCATGAGGCTCCGAACTCCACCTTGGAAAGCGCTTCATCTT 60
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AY402731

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AY402731 936 bp DNA linear GSS 15-DEC-2003
 Mus musculus OR2T10 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION

AY402731 GI:39758714

VERSION

AY402731.1 GI:39758714

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 1 (bases 1 to 936)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Slutsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)

TITLE

Science 302 (5652), 1960-1963 (2003)

JOURNAL

Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Slutsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submision
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

TITLE

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

COMMENT

This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

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 Matches 536; Conservative 0; Mismatches 369; Indels 0; Gaps 0;

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 73 GCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132
 152 CTGCTCTGCGCATGACCATGAGAGCGGCTTCCACATGCTGCTGCTGCTGCTGCT 211
 133 CTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
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LOCUS				
DEFINITION			948 bp DNA linear GSS 12-DEC-2003	
			Homo sapiens HCM3128 gene, VIRTUAL TRANSCRIPT, partial sequence.	
ACCESSION			AY408150	
VERSION			AY408150.1 GI:39764121	
KEYWORDS			GSS.	
SOURCE			Homo sapiens (human)	
ORGANISM			Homo sapiens	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;	
			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE			1 (Bases 1 to 948)	
AUTHORS			Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,	
			Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,	
			Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,	
			Adams,M.D. and Cargill,M.	
TITLE			Infering nonneutral evolution from human-chimp-mouse orthologous	
JOURNAL			gene erios	
PUBMED			Science 302 (5652), 1960-1963 (2003)	
REFERENCE			14671302	
AUTHORS			2 (bases 1 to 948)	
			Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,	
			Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,	
			Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,	
			Adams,M.D. and Cargill,M.	
TITLE			Direct Submission	
JOURNAL			Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	
COMMENT			Rockville, MD 20850, USA	
FEATURES			This sequence was made by sequencing genomic exons and ordering	
			them based on alignment.	
			Location/Qualifiers	

Query Match	31.7%	Score 309.8	DB 29	Length 948
Best Local Similarity	58.9%	Pred. No. 9.5e-77		
Matches 533	Conservative 0	Mismatches 372	Indels 0	Gaps 0

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15 GAACCAATCTTACACAGATGGCTTCTCTTATGAGCATCTTCCACAGATCTGTGTA	74	135	135	100	100
91 TGAATGCTCTATCTCACTTACATTTACATTCCTATATGTTGGCACTGACACCAATGGCT	150	75	75	100	100
151 GGTGCTCTGGCCATCAACATAGAAAGCCGGCTCCACATGGCCCAATGATCTCTGCTTGG	210	135	135	100	100
211 GCAAGCTCTCTCACTGAGACCTCTGTTCACTGTGTGCACTCCCAAGSCCTTGGCGGA	270	195	195	100	100
271 CTTTCTGGCGAGAGAAAACACTATCTCTTTGGAGGCTGTGCACTTCAGATGTTCTGGC	330	255	255	100	100
331 ACTGACATGGGTATGGCGCTGAGGACCTCTCACTGGCCCTTCATGGCCATGACAGGTATGT	390	315	315	100	100
315 TGTCTGTCTTGTGGATTTGAAGGGCTTTGCTGGGAATCAATGGTTATGACCGCTATGT	374	391	391	100	100
375 GGCCATTGTGATCTCTGAAATACATGACCCCTCAATGAGCCCAAGTCTGCTGATCAT	450	435	435	100	100
435 TACTGGAGCTCTCGGGCTTGGGATATGATGATGGCTTGAATCCAGATGGTGTATGAT	494	511	511	100	100
511 GCACCTCCCTTTCTGTGTGTCTCTGGGAATACAGGACCTGCTGTGATCCACCTT	570	495	495	100	100
495 GAATTTCCCTACTGTGGCTTGAGGAAGGTGAACATTTCTTCTGTGAGATCTTATCTT	554	555	555	100	100
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675 TGTGCTGCAAAAGCACTGTCTCAAGGCTTGAAAAAGGCCCTGGCCACCTGTCTCTCCCA	734	751	751	100	100
751 CCTGATTTGTGTGGGATGTTCTATAGAGCTCCACATTCATGTATGTCTTGGCCAGTTTC	810	735	735	100	100
735 CCTGACAGGTGTACACCTCTTCTATAGGGGCAACATGTTCACTTACCTAGGCGTATGAGCA	794	811	811	100	100
811 CTTTCACAGGCCCAACAAGACATCATCTCTGTGTTTCTATACAAATGTGATCTCCACG	870	795	795	100	100
795 CTACGGGGGCCCAAGCCATGACAAAGGTGACCTTATCTTCTACACGGTCTTATCTCCAT	854	871	871	100	100
871 CCTGAATTCATCTATACAGCTTGAAGAAATAGAGGCTCAAGCGGGCCTTGAAGAGGT	930	855	855	100	100
855 GCTCAACCCCTCATTTACAGCTTGAAGAACAGGGAGGTGATGGGGGCACTGAGGAAGGG	914	931	931	100	100
931 CCTGGG 935					

Db 915 GCTGG 919

RESULT 9
AY408151

LOCUS Pan troglodytes HCM3128 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY408151

VERSION AY408151.1 GI:39764122

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 948)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

FEATURES
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Location/Qualifiers
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ORIGIN

Query Match 31.5%; Score 308.2; DB 29; Length 948;
Best Local Similarity 58.8%; Pred. No. 2.7e-76;
Matches 532; Conservative 0; Mismatches 373; Indels 0; Gaps 0;

Db 31 GAATCCACCTGGGAGACGGCTTCATTTGGTGGGATTTGATGACAGTGGCTCC 90
15 GAACCAAGTCTACACAGATGGCTTCTCTGGGCATCTTCCACAGTACTGCTGA 74
91 TGAAGTGTCTAGTCACTTATTAACATCTTATCATGTTGGACCTGACCAATGCT 150
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195 CCAGCTCTCTCTTATGACCTCACTGTTGCTCTGATCAATGTCCTCAAGATGAGCGCA 254
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255 CTTCTGCTGCGAGAGATCTCTCTTCTGAGGCGTGGACATTCAGATGTTCTGGC 314
331 ACTGACATGGGTAGCGCTGAGACCTCTCTACTGCGCTTCTGAGCTTATGACAGATATG 390
315 TGTCTGTTGTGGATCTGAGGGGCTTGTGCTGGGACTATGAGCTTATGACCGCTATGT 374
391 GGCAATTTGTATCTCTGAAATATACATGACCTCTATGAGCCCAAGATCTGCTGATAT 450

Db 375 GGCAATGACACCCACTTACTATCCATCTCTATGATGAGGGCTCTTCCAGAT 434
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435 TACTGGAGCTCTCGGGGCTTTGGGATATGATGATGCTTATCCAGATGGTGTATAT 494
511 GCACCTCCCTTCTGTGTGTCTGGGAAATGAGCATCTGCTGTGAGATCCACCTT 570
495 GAATTTCCCTACTGATGGCTTGAAGAGTGAACCATTTCTTGTGAGATGATACCTT 554
571 GCTGAAGTGGCTCTGTGTGTATACCTCCAGATATGATGATATATACGATGAGATGT 630
555 GTTGAAGCTGGCTGTGTATGACATCTCTGTTGAAGAGTATTTGCTGTCTGTGT 614
631 GACTTCTCTGTGCTCCCATTTTGTGCAATGTGGCCCTCAACACATGATCTATTAC 690
615 CTTATGCTCTCTCTTCCATCTTCCATCATCTGATGAGCTCTCTGATCTTGAAGAC 674
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855 GCTCAACCCCTCTATTACAGCTTGAAGAGAGAGATGATGAGGAGCTGAGAGAGG 914
931 CTTGG 935
915 GCTGG 919

RESULT 10
AY402729

LOCUS Homo sapiens OR2T10 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY402729

VERSION AY402729.1 GI:39758712

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 939)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

FEATURES
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Location/Qualifiers

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ORIGIN

Query Match 30.6%; Score 299.4; DB 29; Length 939;
 Best Local Similarity 57.9%; Pred. No. 8.7e-74;
 Matches 511; Conservative 0; Mismatches 386; Indels 0; Gaps 0;

20 ATGAGAGCTCCGGAACCTCCACCTTGGAGAGCGGCTTCATCTTGGTGGAGATTCGTGAATGAC 79
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Db 901 TTGAAAAAATGCTGAG 917

RESULT 11
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 LOCUS
 DEFINITION

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 Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched
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 homolog [Mus musculus], full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AK053352.1 GI:26343402
 AK053352.1
 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus

REFERENCE

1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtractions of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

TITLE

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtractions of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

3 Shibata, K., Itoh, M., Hayatsu, N., Sugahara, Y., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multiplexed capillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

4 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

TITLE

5 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

JOURNAL

6 (bases 1 to 1931)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanehara, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Harada, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Katsunai, T.,
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
 Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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 Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Yumatsugu, M., and Hayashizaki, Y.

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,

TITLE

Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,

TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,

COMMENT

Kanagawa 230-0045, Japan (E-mail: genome-res@sec.riken.go.jp,
 URL: http://genome.sec.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.sec.riken.go.jp/
 URL: http://fantom.sec.riken.go.jp/
 Location/Qualifiers

FEATURES

source

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CDS

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Query Match 28.6%; Score 279.4; DB 11; Length 1931;
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 Matches 484; Conservative 0; Mismatches 341; Indels 0; Gaps 0;

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 Qy 891 GCCTAGAGAAATTAAGAGATCATGCGGCTTGAAGAGGCTCCG 935
 Db 1611 GCTTGAAGAAACAGGAGGTATGAGGAGCTGAGGAGAAAGACTGG 1655

RESULT 12

AY408152

LOCUS

AY408152 948 bp DNA linear GSS 12-DEC-2003
 DEFINITION Mus musculus Hcm3128 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION

AY408152

VERSION

AY408152.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniensky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

TITLE

JOURNAL

PUBMED

14671302

2 (bases 1 to 948)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniensky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

COMMENT

This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES

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ORIGIN

Query Match 28.1%; Score 274.2; DB 29; Length 948;
 Best Local Similarity 56.6%; Pred. No. 1.4e-66;

QY 501 TGTACTATGACACCTCCCTTCTGTGTCTGTGGAAATCAGGCATCTGCTGTGAGA 560
DB 390 CAGTTGATGTTGTCCTCCCATATGTTGTTCCCGGAAATACCCACCTTTTCTGTATG 449
QY 561 TCCACACCTTGTGAAGTTGGCTGTGTGATACCTCAGGTATAGCTTATATATACG 620
DB 450 TCCCTGACCTTCTCACTCTCAATTCATAGACATGTTGTTGAAAGGTTAAATGTTTA 509
QY 621 TGACAGGTGACATTTCTCTTGTGCTCCCATTTTGCATTTGAGCTTCCCTACACATAG 680
DB 510 TTGTCTGTATATATGTTCTTTTCCCGTAGACATATATGTTCTTCCATGTCCATG 569
QY 681 TCTATTCATCTGTCTGTATGTCATCAATGAGGGAGAGAAAGCCCTTGTACCT 740
DB 570 TTATTAATGCTATCATTTGATGAGATCTGAGAGAGGTCGCGAAAGCTTTTGTACT 629
QY 741 GCTTCTCCACCTATTTGTGTGGGAAATGTTCTATGAGCTGCAATTCATGATGCT 800
DB 630 GTTCTTCCACCTATGTTGTTGTTGAAATGTTATGAGCTGCAATTCATATATATG 689
QY 801 TGCCAGTTCCTTCCAGAGCCCAAGCAACATCATCTCTGTTTCTACACATG 860
DB 690 GGCTGTGTGTCAGACATCCCTTACCGAGCAAGATGTATCAGCCTTACACATCC 749
QY 861 TCACTCCAGCTTGAATTCATCTACAGCTTGAAGATAGAGGTATGCGGCT 920
DB 750 TCACTCCAGCTTGAATTCCTCTCATCTACAGCTTCCGAAACAGAGAGTGCAGAGAT 809
QY 921 TGAGAGAGGT 930
DB 810 TCATGAAGGT 819

RESULT 14
LOCUS BC016940 2021 bp mRNA linear HTC 09-NOV-2001
DEFINITION Homo sapiens, similar to olfactory receptor, family 2, subfamily A,
member 4, clone IMAGE:4424116, mRNA.
ACCESSION BC016940
VERSION BC016940.1 GI:16877381
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 2021)
Strausberg, R.
REFERENCE Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mcddpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: iPAK Plate: 27 Row: 1 Column: 22
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Genomescan gene prediction, Similarity but not identity
to protein
This clone has the following problem: frame shifted.

FEATURES
source
Location/Qualifiers
1..2021
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4424116"
/tissue_type="Kidney, hypernephroma"
/clone_1b="NIH MGC_89"
/lab_host="DH10B"
/note="Vector: pCMV-Sport6"

ORIGIN
Query Match 26.7%; Score 260.6; DB 11; Length 2021;
Best Local Similarity 55.5%; Pred. No. 1.6e-62;
Matches 503; Conservative 0; Mismatches 404; Indels 0; Gaps 0;
38 ACCCTGGAGAGCGCTCATCTGTGGTGGGATTCGTAATGACATGGGCTCTCGAATCG 97
DB 444 ACAATGGTCAACAGGTTCTCTCTCTGAGATTTCTCTGGCCCAAGATTCAGATGCTC 503
QY 98 CTTATGCTACATTTACATCTATACATGTTGGACATGACACAGCAATGCTGTGCTC 157
DB 504 CTTTGTGGGCTCTTCTCCCTGTTTCTATGTCTTACCCCTGCGGGAATGGGACATCCTG 563
QY 158 CTGGCAATACATAGAGAGCCGCTCCACATGCCATGTACTCTCTGTGGGAGCTC 217
DB 564 GGGCTCATCTCAGTGAAGCTCCAGACTCCAGATCCACACCCCATGTACTTCTCTCAACTG 623
QY 218 TCTCTANAGACCTCCCTGTTACATCTGTTGTACTCTCCCAAGGCTTGGCGACTTGTG 277
DB 624 GCGTGTCTCAATGCGCTTATGCTGTGACACAGAGTCCCAAGATCTGTGTAACCTCTG 683
QY 278 CGCAGAGAAAACATATCTCTCTTGGAGCTGTGCACTTCAGATGTTCTTGGACATGCA 337
DB 684 CATCAGCAGCAAGCCATCTCTCTTGTGCGGTGATGACATAGACCTTTCTTTTGTAGT 743
QY 338 ATGGGTAGCGTTGAGACCTCTTACTGCGCTTATAGGCTTATGACAGGTATGTGCCATT 397
DB 744 TTTGCACATCTGATGATGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 803
QY 398 TGTGATCCTCTGAATTCATAGACCTCATAGAGCCCAAGAGTCTGTGATCATGATGAGCC 457
DB 804 TGCCACCTCTCCGATATTTTATATATATGACCTGGAAGATCTGTGATCATCTGTGCCATC 863
QY 458 ACATCTGATATCCGAGCATCCCTGATGCTATAGACATATACATGATCATATGACACTTC 517
DB 864 ACTTCTGAGATGTGCT 923
QY 518 CTTTGTGTGTCTCTGGAATATAGGATGTGCTCTGTGAGATCCACCTTGTGTGAAG 577
DB 924 CCGTTTGTGTGGCTCTGGAATACCACTTCTGTGTGAAATCTGTGTCTCTCTCTCTCT 983
QY 578 TTGGCTGTGTGATCTCTCCAGGTATGAGCTTAAATATAGTGAAGAGTGAAGCTTTC 637
DB 984 CTGGCTGTGTGATCT 1043
QY 638 CTTTGTCTCCCATTTCTGCAATTTGAGCTCTCTACACATGATCTTATGATCTGTGCTT 697
DB 1044 CTGATGGAGACCACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1103
QY 698 CGTATGCCATTAATAGAGGGAGAGAGAAAGCCCTTGTACCTGTCTTCTCCACTGATT 757
DB 1104 AGATATCCAGTCTGGGGAGGGGGCGGAGAAAGCCCTTCTCCACTCTCTCTCCACTCTG 1163
QY 758 GTGGTGGGAGATGTTCTATGAGCTGCCACATTCATGATGATGCTTGGCCAGTCTCTTCAC 817
DB 1164 GTAGTGGAGCTCTTCTTGTGGAGGCGCATGCTCATATGATGAGCCCTTAAGTCCCGCAT 1223
QY 818 AGCCCAAAAGCAACATCATCTCTGTTTCTTACACATTTGTACATCCAGCCCTGAT 877
DB 1224 CCGTAGAGAGAGAGAGGTCTTTTCTATTTTACAGTTCTTTCAACCGATGCTAAAC 1283
QY 878 CCACTCATCTACAGCTGAGGAATAGAGAGTCAATGCGGCTTGAAGAGGATCTCTGGA 937

Db 1284 CCCCTGATTACACCTGAGATGAGAGTCAAGGTCGCTGAGAGACACTGTGC 1343
QY 938 AATACA 944
Db 1344 AAGGAAA 1350

RESULT 15

CE644671/C

LOCUS CE644671 393 bp DNA linear GSS 29-SEP-2003

DEFINITION Cigr-gss-dog-17000367127952 Dog Library Canis familiaris genomic.

ACCESSION CE644671

VERSION CE644671.1 GI:36963091

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 393)

Kirkness, E.F., Batra, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)

MEDLINE 22875432

PUBMED 14512627

COMMENT Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirkness@tigr.org

Class: Shotgun.

Location/Qualifiers

1. 393

/organism="Canis familiaris"

/mol_type="genomic DNA"

/strain="Standard Poodle"

/db_xref="taxon:9615"

/clone_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from

peripheral blood"

ORIGIN

Query Match 26.6%; Score 259.4; DB 29; Length 393;

Best Local Similarity 81.0%; Pred. No. 1.3e-62;

Matches 302; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 552 TGTGAGATGCCACCTGCTGAGAGTGGCTGCTGATACCTCCAGGTATGAGCTTA 611
Db 393 TGTGAGATGCCACCTGCTGAGAGTGGCTGCTGATACCTCCAGGTATGAGCTTA 334
QY 612 TAATATACGTGACAGGTGATGCTTCTCTGCTCCCATTTCTGCAATTGTGACCTCT 671
Db 333 TGTGATGATGATGGGTGATGCTTCTCTGCTCCCATTTCTGCAATTGTGACCTCT 274
QY 672 ACACACTAGTCTTATTCATCTGCTTCTGATGTCATCAATAGAGGAGAAAGCC 731
Db 273 ATACACTAATTTCTGTGATCTGCTTCAATGCTCCCAATGAGGAGAAAGCC 214
QY 732 TTGTACCGTCTCTTCCCACTGATGTTGTTGGAGTGTCTATGAGCTGCCACATTCA 791
Db 213 TAGTACCTGCTCTCTCCCACTGACAGTGTGAGTGTCTTATGAGCTGCCACATTCA 154
QY 792 TGTATGCTTGGCCAGTCTCTTCCACAGCCCAACAGACATCATCTCTGTTTCT 851
Db 153 TGTATGCTCTGCGAGTCTCTTCCCAACAGCCCAACAGACATCATCTCTTCT 94
QY 852 ACACATTGTCACTCAGGCTGATCCACTCATCTACAGCTGAGGAATTAAGAGTCA 911

Db 93 ACACGTTGTCACTCCAGCGTTGAACCCCTTATCTATAGCTGCGAATAAGAGGTCA 34
QY 912 TGCGGCGCTTGAG 924
Db 33 TGGAGCTTGAG 21

Search completed: August 22, 2004, 15:24:59
Job time : 2527 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2004, 08:33:28 ; Search time 93 Seconds

(without alignment)
960.054 Million cell updates/sec

Title: US-10-024-444b-2

Perfect score: 1 MELRNSTLGSGLIVGILND.....VMRALRVLGKYLIAHSTL 316

Sequence: 1 MELRNSTLGSGLIVGILND.....VMRALRVLGKYLIAHSTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1602	100.0	316	4 AAG71681	Aag71681 Human olf
2	1602	100.0	316	5 ABB79908	Abb79908 Human olf
3	1393	87.0	324	4 AAU07088	Aau07088 Human odo
4	1393	87.0	324	5 AAU97928	Aau97928 Novel odo
5	1390	86.8	324	5 AAU97927	Aau97927 Novel odo
6	1390	86.8	316	4 AAG71678	Aag71678 Human olf
7	1390	86.8	316	4 AAU10317	Aau10317 G-protein
8	1390	86.8	316	4 AAU24614	Aau24614 Human olf
9	1390	86.8	316	4 AAU07087	Aau07087 Human odo
10	1390	86.8	316	5 ABP95852	Abp95852 Human GPC
11	1390	86.8	316	5 AAU95574	Aau95574 Human olf
12	1390	86.8	316	5 AAU85234	Aau85234 G-coupled
13	1390	86.8	316	7 ADC85823	Adc85823 Human GPC
14	833	52.0	317	5 ABB81447	Abb81447 Human GPC
15	833	52.0	317	4 AAU24755	Aau24755 Human olf
16	833	52.0	317	5 ABB81446	Abb81446 Human GPC
17	833	52.0	317	5 AAU85375	Aau85375 G-coupled
18	833	52.0	317	6 ABU11174	Abu11174 Human G-P
19	833	52.0	317	7 ADC85549	Adc85549 Human GPC
20	830	51.8	317	5 ABB81455	Abb81455 Human GPC
21	830	51.8	317	5 ABB81456	Abb81456 Human GPC
22	826	51.6	317	5 ABP51586	Abp51586 Human G-P
23	826	51.6	317	5 ABU04732	Abu04732 GPCR 12 p
24	825	51.5	311	4 AAG71713	Aag71713 Human olf
25	825	51.5	318	5 AAU95679	Aau95679 Human olf

26	825	51.5	369	4 AAU24744	Aau24744 Human olf
27	825	51.5	369	5 AAU85364	Aau85364 G-coupled
28	823.5	51.4	324	4 AAU24730	Aau24730 Human olf
29	823.5	51.4	324	5 ABP95871	Abp95871 Human GPC
30	823.5	51.4	324	5 AAU95680	Aau95680 Human olf
31	823.5	51.4	324	5 AAE18655	Aae18655 Human G-P
32	823.5	51.4	324	5 AAU85350	Aau85350 Human G-P
33	819.5	51.2	321	4 AAG71467	Aag71467 Human olf
34	817	51.0	313	6 ABR01652	Abt01652 Human G-P
35	816	50.9	314	4 AAG71794	Aag71794 Human olf
36	816	50.9	314	4 AAG71902	Aag71902 Human olf
37	816	50.9	314	4 AAE06762	Aae06762 Human G-P
38	816	50.9	314	4 AAU05138	Aau05138 Human odo
39	816	50.9	314	4 AAU24587	Aau24587 Human olf
40	816	50.9	314	5 ABU04025	Abu04025 Human G-P
41	816	50.9	314	5 ABP95895	Abp95895 Human GPC
42	816	50.9	314	5 AAU95551	Aau95551 Human olf
43	816	50.9	314	5 AAU85207	Aau85207 G-coupled
44	816	50.9	314	7 ADC86135	Adc86135 Human GPC
45	816	50.9	317	4 AAU05139	Aau05139 Human odo

ALIGNMENTS

RESULT 1
AAG71681
ID AAG71681 standard; protein, 316 AA.

AC AAG71681;
XX
XX
XX 30-JUL-2001 (first entry)
XX
XX
XX Human olfactory receptor polypeptide, SEQ ID NO: 1362.

DE Human olfactory receptor polypeptide, SEQ ID NO: 1362.
XX
XX
XX Human, olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
XX scent profile; scent fingerprint; scent representation.

XX OS Homo sapiens.

XX PN W0200127158-A2.

XX PD 19-APR-2001.

XX PF 06-OCT-2000; 2000WO-US027582.

XX PR 08-OCT-1999; 99US-0158615P.

XX PR 24-FEB-2000; 2000US-0184809P.

XX PA (DIGI-) DIGISCENTS.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Bellenson J, Smith D, Lancel D, Glusman G, Fuchs T, Yanai I,

XX DR WPI; 2001-290713/30.

XX XX New polynucleotides which encode polypeptides involved in olfactory

XX PT sensation for identifying olfactory agonists and antagonists.

XX PS Claim 11; Page 845; 1857pp; English.

XX The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be

CC used for determining differences in the olfactory faculties of different individuals

XX Sequence 316 AA:

Query Match 100.0%; Score 1602; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 5.5e-167; Mismatches 0; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELNSTLGGSGFIIVGILINDSGSPPELLYATFTITVMTALTSNGILLAITTEARLHMPY 60
DB 1 MELNSTLGGSGFIIVGILINDSGSPPELLYATFTITVMTALTSNGILLAITTEARLHMPY 60
QY 61 LLLGQLSLMDLIFTSVTPPKALADPLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
DB 61 LLLGQLSLMDLIFTSVTPPKALADPLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
QY 121 DRYVAICHPKMTLMSPRVCIMVATSMILASLAIAGHTWTMHLPCVSWEIRHLCE 180
DB 121 DRYVAICHPKMTLMSPRVCIMVATSMILASLAIAGHTWTMHLPCVSWEIRHLCE 180
QY 181 IPLLKACADTSRYELIIVYGVTFLLPISAIYASTVLVFTVLRMPSNNGRKKALVT 240
DB 181 IPLLKACADTSRYELIIVYGVTFLLPISAIYASTVLVFTVLRMPSNNGRKKALVT 240
QY 241 CSSHIIIVGMFGATFMVVLPSFSHPKODNIIISVFTITVPALNPLIYSLRNKEVMA 300
DB 241 CSSHIIIVGMFGATFMVVLPSFSHPKODNIIISVFTITVPALNPLIYSLRNKEVMA 300
QY 301 LRRVLGKYILLAHSTL 316
DB 301 LRRVLGKYILLAHSTL 316

RESULT 2

ID ABB79908 standard; protein; 316 AA.

XX ABB79908;

XX 05-DEC-2002 (first entry)

XX Human olfactory receptor-like protein GPCR1.

XX GPCR1, olfactory receptor; G-protein coupled receptor; receptor; human;

XX antiarteriosclerotic; antidiabetic; analgesic; cytosstatic;

XX antiatherogenic; neurotrophic; neuroprotective; immunosuppressive;

XX antiatherogenic; neurotrophic; neuroprotective; immunosuppressive;

XX cardiomyopathy; atherosclerosis; diabetes; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 41..290

XX /note= "7tm_1 domain"

XX WO00270707-A2.

XX 12-SEP-2002.

XX 18-DEC-2001; 2001WO-US049168.

XX 18-DEC-2000; 2000US-0256635P.

XX (CURA-) CURAGEN CORP.

XX (CORT-) COR THERAPEUTICS INC.

XX Padigaru M., Gerlach V., Smithson G., Stone D., Bin-Yang R.,

XX Conley P., Hart M., Tomlinson JE., Topper UN., Kekuda R., Casman SJ,

XX Edinger S., Macdougall JR;

XX WPI; 2002-698753/75.

XX N-PSDB; ABQ81238.

XX New G-protein coupled receptor (GPCR1) proteins and nucleic acids, useful
PT for treating or preventing a GPCR1-associated disorder, e.g.
PT cardiomyopathy, atherosclerosis, diabetes, or disorders related to cell
PT signal processing.

XX Claim 1; Page 11; 11np; English.

CC The present sequence is the protein sequence of a novel human G-protein
CC coupled receptor, designated GPCR1, that has structural and physiological
CC functions characteristic of the olfactory receptor family, and has
CC properties similar to those of proteins containing the 7tm_1 7
CC transmembrane receptor (rhodopsin family). The invention provides GPCR1
CC polypeptides and nucleic acids, and methods for their recombinant
CC production. These are useful for treating or preventing a GPCR1-
CC associated disorder, such as cardiomyopathy, atherosclerosis, diabetes,
CC or a disorder related to cell signal processing or metabolic pathway
CC modulation in humans (claimed). They may further be used for treating or
CC preventing e.g. developmental diseases, metabolic pathway disorders,
CC retinal disorders, wasting disorders associated with chronic diseases,
CC pain, cancer, psychotic and neurological disorders (e.g. anxiety or
CC schizophrenia), autoimmune diseases, allergies, bacterial, fungal,
CC protozoal and viral infections, neurodegenerative diseases (e.g.
CC Alzheimer's disease), and hematopoietic diseases. The proteins and
CC nucleic acids may also be used as research tools, as diagnostic or
CC prognostic markers, in gene therapy, for promoting tissue regeneration in
CC vitro and in vivo, and as biological defence weapons. The proteins are
CC also useful for producing antibodies specific for the proteins, as
CC vaccines, and in screening for potential agonists and antagonists

XX Sequence 316 AA:

Query Match 100.0%; Score 1602; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 5.5e-167; Mismatches 0; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELNSTLGGSGFIIVGILINDSGSPPELLYATFTITVMTALTSNGILLAITTEARLHMPY 60
DB 1 MELNSTLGGSGFIIVGILINDSGSPPELLYATFTITVMTALTSNGILLAITTEARLHMPY 60
QY 61 LLLGQLSLMDLIFTSVTPPKALADPLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
DB 61 LLLGQLSLMDLIFTSVTPPKALADPLRENTISFGGCAQMFALMTGSAEDLLAFMAY 120
QY 121 DRYVAICHPKMTLMSPRVCIMVATSMILASLAIAGHTWTMHLPCVSWEIRHLCE 180
DB 121 DRYVAICHPKMTLMSPRVCIMVATSMILASLAIAGHTWTMHLPCVSWEIRHLCE 180
QY 181 IPLLKACADTSRYELIIVYGVTFLLPISAIYASTVLVFTVLRMPSNNGRKKALVT 240
DB 181 IPLLKACADTSRYELIIVYGVTFLLPISAIYASTVLVFTVLRMPSNNGRKKALVT 240
QY 241 CSSHIIIVGMFGATFMVVLPSFSHPKODNIIISVFTITVPALNPLIYSLRNKEVMA 300
DB 241 CSSHIIIVGMFGATFMVVLPSFSHPKODNIIISVFTITVPALNPLIYSLRNKEVMA 300
QY 301 LRRVLGKYILLAHSTL 316
DB 301 LRRVLGKYILLAHSTL 316

RESULT 3

ID AAU07088 standard; protein; 324 AA.

XX AAU07088;

XX 24-OCT-2001 (first entry)

XX Human odorant receptor (OR) polypeptide #5.

XX Human, olfactory receptor; OR; G-protein coupled receptor superfamily;

XX GPCR; gene therapy; tranquiliser; vulnerary; anti-HIV; cytosstatic;

XX KW

KM nootropic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;
 KM antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;
 KM human immunodeficiency virus; neoplastic growth; neurological disorder;
 KM Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;
 KM wound healing; asthma; Albright hereditary osteodystrophy;
 KM multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.
 OS Homo sapiens.
 XX MO200157215-A2.
 PN 09-AUG-2001.
 PD 07-FEB-2001; 2001WO-US003923.
 PP 07-FEB-2000; 2000US-0180511P.
 PR 07-FEB-2000; 2000US-0180630P.
 PR 07-FEB-2000; 2000US-0180646P.
 PR 08-FEB-2000; 2000US-0180930P.
 PR 08-FEB-2000; 2000US-0181004P.
 PR 08-FEB-2000; 2000US-0181013P.
 PR 08-FEB-2000; 2000US-0181043P.
 PR 24-JUL-2000; 2000US-0220262P.
 PR 25-JUL-2000; 2000US-0220594P.
 PR 11-AUG-2000; 2000US-0224596P.
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-0077789.
 XX (CURA-) CURAGEN CORP.
 PA Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS;
 PI Baumgartner JC;
 PI MPI; 2001-488883/53.
 DR N-PSDB; AAS11688.
 DR Novel isolated NOVX polypeptide related to human odorant receptor family
 PT of G-protein coupled receptor superfamily of proteins useful for treating
 PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
 XX
 PS Claim 1; Page 44; 199pp; English.
 CC Novel isolated NOVX polynucleotides and their encoded polypeptides of the
 CC invention are related to the human olfactory (or odorant) receptors
 CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
 CC sequences are useful for treating or preventing a pathology associated
 CC with OR in a subject, and for manufacturing a medicament for treating a
 CC syndrome associated with a human disease. These diseases include
 CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
 CC growth, neurological disorders, such as Parkinson's disease and
 CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
 CC disease, multiple sclerosis, and Albright hereditary osteodystrophy. The
 CC polynucleotides and polypeptides are also useful, to identify proteins of
 CC the same family, to screen for molecules which inhibit or enhance the
 CC activity or function of olfactory receptors, to detect nasal epithelial
 CC neuronal tissue, in production of transgenic plants and for the
 CC development of new drug targets for various disorders. This sequence
 CC represents a human OR polypeptide
 XX
 SQ Sequence 324 AA;
 Query Match 87.0%; Score 1393; DB 4; Length 324;
 Best Local Similarity 87.3%; Pred. No. 4.9e-144;
 Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 121 DRYVALCHPLKXTMLSPBVCWIMVATSWILASLIALGHNTMTMLPFCVSMETRIHLCE 180
 Db 129 DRYVALCHPLKXTMLSPBVCWIMVATSWILASLIALGHNTMTMLPFCVSMETRIHLCE 188
 QY 181 IPEPLKLAADNTSYELIYVTGTPLLPISAVASYTLVLPYLRBPSNEGRKALVT 240
 Db 189 IPEPLKLAADNTSYELIYVTGTPLLPISAVASYTLVLPYLRBPSNEGRKALVT 248
 QY 241 CSNLIYVGMFYGATMYVLPSSFSHPKDNISVFYITVPALNPLIYSLRNKEVRA 300
 Db 249 CSNLIYVGMFYGATMYVLPSSFSHPKDNISVFYITVPALNPLIYSLRNKEVRA 308
 QY 301 LRRVLKXTLLAHSSTL 316
 Db 309 LRRVLKXTLLAHSSTL 324
 RESULT 4
 AAU97928 standard; protein, 324 AA.
 AAU97928;
 15-AUG-2002 (first entry)
 DE Novel odourant receptor NOV7 protein.
 KM NOX; odorant receptor; G protein coupled receptor; GPCR; trauma;
 KM olfactory receptor; olfactory loss; neoplastic growth;
 KM human immunodeficiency virus; Alzheimer's disease; HIV;
 KM neurological disorder; Parkinson's disease.
 OS Unidentified.
 XX
 PN WO200236632-A2.
 PD 10-MAY-2002.
 PF 09-OCT-2001; 2001WO-US031744.
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-0077789.
 PR 20-SEP-2001; 2001US-00245292.
 PA (CURA-) CURAGEN CORP.
 PI Alsobrook JP, Burgess CE, Grosse WM, Lepley DM, Padigaru M;
 PI Spytek KA;
 PI MPI; 2002-471499/50.
 DR N-PSDB; ABEK51097.
 DR New isolated olfactory receptor-like polypeptide, NOVX, useful for
 PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
 PT trauma, human immunodeficiency virus illness, neoplastic growth and
 PT neurological disorders.
 XX
 PS Claim 1; Page 34-35; 122pp; English.
 CC This invention relates to the DNA and protein sequences of a novel
 CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
 CC sequences of the invention and an antibody specific for the protein are
 CC useful for treating or preventing a disorder associated with NOVX in a
 CC subject, preferably human. A NOVX specific antibody is useful for
 CC determining the presence or amount of protein in a sample. The DNA,
 CC protein and antibody of the invention is useful for diagnosing,
 CC preventing or treating disorders associated with aberrant NOVX expression
 CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
 CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
 CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
 CC antibody is useful in screening assays, detection assays (e.g.,
 CC chromosome mapping, tissue typing, forensic biology), predictive
 CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical

CC trials and pharmacogenomic), and in methods of treatment (e.g.,
CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC produce antibodies immunospecific for the protein, to screen for
CC potential agonist and antagonist compounds, and as bait protein in a two-
CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
CC invention is useful for isolating, and purifying the protein and to
CC monitor protein levels in tissue as part of a clinical testing procedure.
CC The present sequence represents the NOV7 protein of the invention
XX

Sequence 324 AA:

Query Match 87.0%; Score 1393; DB 5; Length 324;
Best Local Similarity 87.3%; Pred. No. 4.9e-144;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLVGLINDSGSPPELLVATFTIYMLALTSNGILLATTEARLHMPY 60
DB 9 MELMNTLGGFLVGLINDSGSPPELLCATITTIYLLALISNGLLALITMEARLHMPY 68
QY 61 LILGQLSLMDLFTSVTPKALADFLRRNTISFGGCAQMFALTMGSAEDILLAFMAY 120
DB 69 LILGQLSLMDLFTSVTPKALADFLRRNTISFGGCAQMFALTMGSAEDILLAFMAY 128
QY 121 DRYVALCHPLKWTMTSPRCVMTVAATSWILASLAIAGHTMYTMHLPCVSWERHLLCE 180
DB 129 DRYVALCHPLKWTMTMTSSRCVMTVAATSWILASLAIAGHTMYTMHLPCVSWERHLLCE 188
QY 181 IPELKLACADTSRYELIYVGVTELLPISAIYASVTLVFTVLRMPSNEGRKALVT 240
DB 189 IPELKLACADTSRYELIYVGVTELLPISAIYASVTLVFTVLRMPSNEGRKALVT 248
QY 241 CSSHLTVGMFGAATFMYVLPSSFSKPDNIISVFTIIVPALNPLIYSLNKEVMA 300
DB 249 CSSHLTVGMFGAATFMYVLPSSFSKPDNIISVFTIIVPALNPLIYSLNKEVMA 308
QY 301 LRRVLGKYTLIAHSTL 316
DB 309 LRRVLGKYTLIAHSTL 324

RESULT 5
AAU97927
ID AAU97927 standard; protein; 324 AA.
XX

AAU97927;

15-AUG-2002 (first entry)

Novel odourant receptor NOV6 protein.

NOV, odorant receptor; G protein coupled receptor; GPCR; trauma;
olfactory receptor; olfactory loss; neoplastic growth;
human immunodeficiency virus; Alzheimer's disease; HIV;
neurological disorder; Parkinson's disease.

Unidentified.

WO200236632-A2.

10-MAY-2002.

09-OCT-2001; 2001WO-US031744.

02-NOV-2000; 2000US-0245292P.

06-FEB-2001; 2001US-0077789.

20-SEP-2001; 2001US-00245292.

(CURA-) CURAGEN CORP.
Alsedbrook JP, Burgess CE, Grosse WM, Lepley DM, Padigaru M,
Spytek KA;

XX WPI: 2002-471499/50.
DR N-P-SDB; ABK53096.

XX New isolated olfactory receptor-like polypeptide, NOVX, useful for
PT diagnosing, preventing or treating disorders of olfactory loss, e.g.
PT trauma, human immunodeficiency virus illness, neoplastic growth and
PT neurological disorders.

PS Claim 1; Page 33; 122pp; English.

XX This invention relates to the DNA and protein sequences of a novel
CC isolated olfactory receptor-like polypeptide, NOVX. The DNA and protein
CC sequences of the invention and an antibody specific for the protein are
CC useful for treating or preventing a disorder associated with NOV1 in a
CC subject, preferably human. A NOVX specific antibody is useful for
CC determining the presence or amount of protein in a sample. The DNA,
CC protein and antibody of the invention is useful for diagnosing,
CC preventing or treating disorders associated with aberrant NOVX expression
CC such as disorders of olfactory loss, e.g. trauma, human immunodeficiency
CC virus (HIV) illness, neoplastic growth and neurological disorders, e.g.
CC Parkinson's disease and Alzheimer's disease. The sequences and NOV
CC antibody is useful in screening assays, detection assays (e.g.,
CC chromosomal mapping, tissue typing, forensic biology), predictive
CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
CC trials and pharmacogenomic), and in methods of treatment (e.g.,
CC therapeutic and prophylactic). The NOV protein is useful as immunogen to
CC produce antibodies immunospecific for the protein, to screen for
CC potential agonist and antagonist compounds, and as bait protein in a two-
CC hybrid or three-hybrid assay. The nucleotide sequence is useful in gene
CC therapy, to express the protein, to detect NOVX mRNA or a genetic lesion
CC in a NOVX gene, and to modulate NOVX activity. The antibody of the
CC invention is useful for isolating, and purifying the protein and to
CC monitor protein levels in tissue as part of a clinical testing procedure.
CC The present sequence represents the NOV6 protein of the invention
XX

Sequence 324 AA:

Query Match 87.0%; Score 1393; DB 5; Length 324;
Best Local Similarity 87.3%; Pred. No. 4.9e-144;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLVGLINDSGSPPELLVATFTIYMLALTSNGILLATTEARLHMPY 60
DB 9 MELMNTLGGFLVGLINDSGSPPELLCATITTIYLLALISNGLLALITMEARLHMPY 68
QY 61 LILGQLSLMDLFTSVTPKALADFLRRNTISFGGCAQMFALTMGSAEDILLAFMAY 120
DB 69 LILGQLSLMDLFTSVTPKALADFLRRNTISFGGCAQMFALTMGSAEDILLAFMAY 128
QY 121 DRYVALCHPLKWTMTSPRCVMTVAATSWILASLAIAGHTMYTMHLPCVSWERHLLCE 180
DB 129 DRYVALCHPLKWTMTMTSSRCVMTVAATSWILASLAIAGHTMYTMHLPCVSWERHLLCE 188
QY 181 IPELKLACADTSRYELIYVGVTELLPISAIYASVTLVFTVLRMPSNEGRKALVT 240
DB 189 IPELKLACADTSRYELIYVGVTELLPISAIYASVTLVFTVLRMPSNEGRKALVT 248
QY 241 CSSHLTVGMFGAATFMYVLPSSFSKPDNIISVFTIIVPALNPLIYSLNKEVMA 300
DB 249 CSSHLTVGMFGAATFMYVLPSSFSKPDNIISVFTIIVPALNPLIYSLNKEVMA 308
QY 301 LRRVLGKYTLIAHSTL 316
DB 309 LRRVLGKYTLIAHSTL 324

RESULT 6
AAG71678
ID AAG71678 standard; protein; 316 AA.
XX

AAG71678;

DT 30-JUN-2001 (first entry)
 XX Human olfactory receptor polypeptide, SEQ ID NO: 1359.
 DE
 XX Human, olfactory receptor; OR: primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KM scent profile; scent fingerprint; scent representation.
 XX
 OS Homo sapiens.
 XX
 PN MO200127158-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US027582.
 XX
 PR 08-OCT-1999; 99US-0158615P.
 PR 24-FEB-2000; 2000US-0184809P.
 XX
 PA (DIGI-) DIGISCENTS.
 XX (YEDA) YEDA RES & DEV CO LTD.
 PI
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 DR MPI; 2001-290713/30.
 XX
 XX New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.
 XX
 PS Claim 11; Page 842-843; 1857PP; English.
 XX
 XX The present sequence is an olfactory receptor which is encoded by one of
 CC a number of novel polynucleotides. The polynucleotides can be used in
 CC screening for olfactory agonists and antagonists. The methods allow for
 CC the determination of primary scents and the identification of the odour
 CC receptors used to detect these primary scents. The methods also enable
 CC determination of secondary scents and the identification of combinations
 CC of odour receptors that are involved in detecting such secondary scents.
 CC This enables the construction of a scent representation (also called a
 CC scent fingerprint or scent profile), which may be used to re-create and
 CC edit scents. Libraries of olfactory receptors are useful for determining
 CC the interaction pattern of a composition with the receptors, and can be
 CC used for determining differences in the olfactory faculties of different
 CC individuals
 CC
 XX Sequence 316 AA;
 SQ
 Query Match 86.8%; Score 1390; DB 4; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;
 Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

DB 301 LRRVLGKXMLPAHSTL 316
 RESULT 7
 AAU10317
 ID AAU10317 standard; protein; 316 AA.
 XX
 XX AAU10317;
 XX
 DT 25-JAN-2002 (first entry)
 XX
 DE G-protein coupled receptor (GCRC) #18.
 XX
 KW G-protein coupled receptor; GCRC; vaccine; gene therapy;
 KW cell proliferation disorder; cancer; arteriosclerosis;
 KW neurological disorder; epilepsy; stroke; cardiovascular disorder;
 KW hypertension; ischemic heart disease; gastrointestinal disorder;
 KW anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
 KW diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
 KW schizophrenic disorder; neuroskeletal disorder.
 XX
 OS Homo sapiens.
 XX
 PN MO20016742-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001WO-US006814.
 XX
 PR 03-MAR-2000; 2000US-0186854P.
 PR 10-MAR-2000; 2000US-0188384P.
 PR 17-MAR-2000; 2000US-0190453P.
 PR 20-MAR-2000; 2000US-0190730P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lal P, Tang YT, Patterson C, Yao MG, Shih LU, Tribouley CM;
 PI Lu DM, Yue H, Khan FA, Pollocky JL, Au-Young J, Yang J, Harland L;
 PI Walsh RT, Lo TP, Borowsky ML;
 DR MPI; 2001-656776/75.
 DR N-PSDB; AAS15914.
 XX
 PT Novel G-protein coupled receptor polypeptides, for treating and
 PT preventing autoimmune/inflammatory disorders, neurological disorders,
 PT cell proliferative disorders, cardiovascular disorders and viral
 PT infections.
 XX
 PS Claim 1; Page 128; 141pp; English.
 XX
 XX The invention describes a novel isolated polypeptide, selected from a
 CC group of 21 G-protein coupled receptor polypeptides (GCRC) and useful in
 CC vaccines and gene therapy. The polypeptide (I) is useful for screening
 CC for agonist or antagonist of (I), compounds specifically binding to (I),
 CC or compounds that modulate the activity of (I). The polynucleotide
 CC encoding (I) is useful for screening a compound for effectiveness in
 CC altering expression of a target polynucleotide comprising (II), by
 CC exposing a sample comprising the target polynucleotide to a compound,
 CC detecting altered expression of the target polynucleotide, and comparing
 CC the expression of the target polynucleotide in the presence of varying
 CC amounts of compound and in the absence of the compound. (I) and (II) are
 CC useful for diagnosis, treatment and prevention of cell proliferative
 CC disorders (e.g. cancers, arteriosclerosis, atherosclerosis), neurological
 CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and
 CC neuroskeletal disorders), cardiovascular disorders (e.g. hypertension,
 CC ischemic heart disease), gastrointestinal disorders (e.g. anorexia,
 CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,
 CC osteoporosis, psoriasis), and metabolic disorders such as obesity.
 CC Furthermore, the polynucleotide is useful as primers for detecting
 CC single nucleotide polymorphisms; as elements in microarrays, to monitor or
 CC measure protein-protein interactions, drug-target interactions, and gene
 CC expression profiles; to generate a transcript image of a tissue or cell
 CC type, and to generate hybridisation probes useful in mapping the

CC naturally occurring genomic sequence. This is the G-protein coupled
 CC receptor 18 (GPRC-18), one of 21 GPCR proteins described in the method
 CC of the invention

XX
 XX
 SQ Sequence 316 AA;

Query Match 86.8%; Score 1390; DB 4; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;
 Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLVGLINDSGPELLIYATFTLLIYMLALNSGLLAIITTEARLHMPY 60
 DB 1 MELRNFTLGGFLVGLINDSGPELLIYATFTLLIYMLALNSGLLAIITTEARLHMPY 60
 QY 61 LLLGQSLMDLFTSVTPRALADFLRENTISFGGALQMFALITMGSAEDLLAFMAY 120
 DB 61 LLLGQSLMDLFTSVTPRALADFLRENTISFGGALQMFALITMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPLKMYTLMSPRCWIMVATSWILASLIAIGHTMYTMLPFCVSWIEIRHLICE 180
 DB 121 DRYVAICHPLKMYTLMSPRCWIMVATSWILASLIAIGHTMYTMLPFCVSWIEIRHLICE 180
 QY 181 IPPLLKACADTSREYELIYVTGTFLLIPSAIVASYTLVLTFLMPSNEGRKKALVT 240
 DB 181 IPHLLKACADTSREYELIYVTGTFLLIPSAIVASYTLVLTFLMPSNEGRKKALVT 240
 QY 241 CSSHLYVGMFYGAATFMYVLPSSFHSPKQDNISVFYITVPALNPLIYSLRNKEVWRA 300
 DB 241 CSSHLYVGMFYGAATFMYVLPSSFHSPKQDNISVFYITVPALNPLIYSLRNKEVWRA 300
 QY 301 LRRVLGKXYLLAHSTL 316
 DB 301 LRRVLGKXYLLAHSTL 316

RESULT 8

ID AAU24614 standard; protein; 316 AA.

XX AAU24614;
 AC 18-DEC-2001 (first entry)
 DT Human olfactory receptor AOLFRL07.
 DE Human olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 KW food additive; cosmetic; fragrance; pharmaceutical additive.
 KM
 KW
 XX Homo sapiens.

OS

WO200168805-A2.

PD 20-SEP-2001.

PF 13-MAR-2001; 2001WO-US007771.

PR 13-MAR-2000; 2000US-0188914P.

PR 24-MAR-2000; 2000US-0192033P.

PR 12-APR-2000; 2000US-0198474P.

PR 24-APR-2000; 2000US-0199335P.

PR 26-MAY-2000; 2000US-0207702P.

PR 23-JUN-2000; 2000US-0213849P.

PR 16-AUG-2000; 2000US-0226534P.

PR 07-SEP-2000; 2000US-0230732P.

PR 07-FEB-2001; 2001US-0266862P.

(SENO-) SENOMYX INC.

Zozulya S;

WPI, 2001-570867/64.

DR N-PSDB; AAS42307.

PT Nucleic acids encoding human olfactory G protein-coupled receptors,
 PT useful for screening for compounds involved in olfactory sensation, where
 PT the compounds can be used in the food, pharmaceutical and cosmetic
 PT industries to customize odors.

PS Claim 60; Page 127; 319pp; English.

XX The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence is a human olfactory receptor of the
 CC invention

XX
 SQ Sequence 316 AA;

Query Match 86.8%; Score 1390; DB 4; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;
 Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLVGLINDSGPELLIYATFTLLIYMLALNSGLLAIITTEARLHMPY 60
 DB 1 MELRNFTLGGFLVGLINDSGPELLIYATFTLLIYMLALNSGLLAIITTEARLHMPY 60
 QY 61 LLLGQSLMDLFTSVTPRALADFLRENTISFGGALQMFALITMGSAEDLLAFMAY 120
 DB 61 LLLGQSLMDLFTSVTPRALADFLRENTISFGGALQMFALITMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPLKMYTLMSPRCWIMVATSWILASLIAIGHTMYTMLPFCVSWIEIRHLICE 180
 DB 121 DRYVAICHPLKMYTLMSPRCWIMVATSWILASLIAIGHTMYTMLPFCVSWIEIRHLICE 180
 QY 181 IPPLLKACADTSREYELIYVTGTFLLIPSAIVASYTLVLTFLMPSNEGRKKALVT 240
 DB 181 IPHLLKACADTSREYELIYVTGTFLLIPSAIVASYTLVLTFLMPSNEGRKKALVT 240
 QY 241 CSSHLYVGMFYGAATFMYVLPSSFHSPKQDNISVFYITVPALNPLIYSLRNKEVWRA 300
 DB 241 CSSHLYVGMFYGAATFMYVLPSSFHSPKQDNISVFYITVPALNPLIYSLRNKEVWRA 300
 QY 301 LRRVLGKXYLLAHSTL 316
 DB 301 LRRVLGKXYLLAHSTL 316

RESULT 9

ID AAU07087 standard; protein; 316 AA.

AC AAU07087;

DT 24-OCT-2001 (first entry)

DE Human odorant receptor (OR) polypeptide #4.

DE Human olfactory receptor; OR; G-protein coupled receptor superfamily;

KW GPCR; gene therapy; tranquilliser; vulnerary; anti-HIV; cytostatic;

KW nocotropic; neuroprotective; antiparkinsonian; antiasthmatic; cancer;

KW antiinflammatory; odorant receptor; olfactory loss; trauma; HIV;

KW human immunodeficiency virus; neoplastic growth; neurological disorder;

KW Parkinson's disease; Alzheimer's disease; neurogenesis; Crohn's disease;

KW wound healing; asthma; Albigier hereditary osteodysplrophy;
 KW multiple sclerosis; nasal epithelial neuronal tissue; transgenic plant.

XX Homo sapiens.

OS

WO200157215-A2.

PD 09-AUG-2001.
 XX 07-FEB-2001; 2001WO-US003923.
 PF 07-FEB-2000; 2000US-0180511P.
 XX 07-FEB-2000; 2000US-0180630P.
 PR 07-FEB-2000; 2000US-0180630P.
 PR 08-FEB-2000; 2000US-0180930P.
 PR 08-FEB-2000; 2000US-0181004P.
 PR 08-FEB-2000; 2000US-0181013P.
 PR 08-FEB-2000; 2000US-0181043P.
 PR 24-JUL-2000; 2000US-0220262P.
 PR 25-JUL-2000; 2000US-0220594P.
 PR 11-AUG-2000; 2000US-0224596P.
 PR 02-NOV-2000; 2000US-0245292P.
 PR 06-FEB-2001; 2001US-00777789.
 XX (CURA-) CURAGEN CORP.
 PA Padigaru M, Spytek KA, Li L, Ballinger RA, Mishra VS,
 PI Baumgartner JC;
 PI WPI; 2001-488883/53.
 DR N-PSDB; AAS11687.
 DR N-PSDB; AAS11687/53.
 XX Novel isolated NOVX polypeptide related to human odorant receptor family
 PT of G-protein coupled receptor superfamily of proteins useful for treating
 PT trauma, neoplastic growth, Parkinson's disease, Alzheimer's disease.
 XX Claim 1; Page 39; 199pp; English.
 XX Novel isolated NOVX polynucleotides and their encoded polypeptides of the
 CC invention are related to the human olfactory (or odorant) receptors
 CC (ORs), from the G-protein coupled receptor (GPCR) superfamily. The
 CC sequences are useful for treating or preventing a pathology associated
 CC with OR in a subject, and for manufacturing a medicament for treating a
 CC syndrome associated with a human disease. These diseases include
 CC disorders of olfactory loss, such as trauma, HIV illness and neoplastic
 CC growth, neurological disorders, such as Parkinson's disease and
 CC Alzheimer's disease, neurogenesis, cancer, wound healing, asthma, Crohn's
 CC disease, multiple sclerosis, and Abright hereditary osteodys trophy. The
 CC polynucleotides and polypeptides are also useful, to identify proteins of
 CC the same family, to screen for molecules which inhibit or enhance the
 CC activity or function of olfactory receptors, to detect nasal epithelial
 CC neuronal tissue, in production of transgenic plants and for the
 CC development of new drug targets for various disorders. This sequence
 CC represents a human OR polypeptide
 XX
 XX Sequence 316 AA;
 SQ
 Query Match 86.8%; Score 1390; DB 4; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;
 Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;
 QY 1 MELRNSTGSGFLVGIINDSGSPFLVATFTILVWALTSNGLLATITRARLMPY 60
 DB 1 MELRNFTGSGFLVGIINDSGSPFLCATITILVLAISGCLLATITMARLMPY 60
 QY 61 LILGQLSMDLLFTSVTPKALADFLRRENTISFGSCALQMFALATMGSAEDLLAFMAY 120
 DB 61 LILGQLSMDLLFTSVTPKALADFLRRENTISFGSCALQMFALATMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPILKMTLMSRVCWIMVATSWIIASLAIQHTWTWMLPCVSWEIRHLCE 180
 DB 121 DRYVAICHPILKMTLMSRVCWIMVATSWIIASLAIQHTWTWMLPCVSWEIRHLCE 180
 QY 181 IPEPLKACADTSRELIIVYGVTEFLPISAIYASVTLVFTLRLMPSNGRKAIVT 240
 DB 181 IPEPLKACADTSRELIIVYGVTEFLPISAIYASVTLVFTLRLMPSNGRKAIVT 240
 QY 241 CSSHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFYITVTPALNPLIYSIRKENVRA 300
 DB 241 CSSHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFYITVTPALNPLIYSIRKENVRA 300

QY 301 LRRVLGKXIIIAHSTL 316
 DB 301 LRRVLGKXIIIAHSTL 316
 RESULT 10
 ID ABP95852 standard; protein; 316 AA.
 XX ABP95852;
 AC ABP95852;
 XX 06-MAR-2003 (first entry)
 DT Human GPCR polypeptide SEQ ID NO 514.
 DE Human GPCR; G protein coupled receptor; signal transduction; olfactory;
 XX drug development; gustatory; taste; fragrance; receptor.
 OS Homo sapiens.
 XX WO200216548-A2.
 EN 28-FEB-2002.
 PD 30-JUL-2001; 2001WO-IB001446.
 PF 04-AUG-2000; 2000JP-00237818.
 PR 13-FEB-2001; 2001JP-00034434.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA Haga T, Takeda S, Mitaku S;
 PI WPI; 2002-304118/34.
 DR N-PSDB; AB243126.
 XX Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 XX Claim 10; SEQ ID NO 514; 97pp + Sequence Listing; Japanese.
 XX The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (AB242870-AB243126) and/or GPCR proteins (ABP95596-
 CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets
 CC for drug development e.g. based on olfactory and gustatory receptors in
 CC form of agonists and antagonists by screening intrinsic and extrinsic
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIP0 at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 316 AA;
 SQ
 Query Match 86.8%; Score 1390; DB 5; Length 316;
 Best Local Similarity 87.0%; Pred. No. 1e-143;
 Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;
 QY 1 MELRNSTGSGFLVGIINDSGSPFLVATFTILVWALTSNGLLATITRARLMPY 60
 DB 1 MELRNFTGSGFLVGIINDSGSPFLCATITILVLAISGCLLATITMARLMPY 60
 QY 61 LILGQLSMDLLFTSVTPKALADFLRRENTISFGSCALQMFALATMGSAEDLLAFMAY 120
 DB 61 LILGQLSMDLLFTSVTPKALADFLRRENTISFGSCALQMFALATMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPILKMTLMSRVCWIMVATSWIIASLAIQHTWTWMLPCVSWEIRHLCE 180
 DB 121 DRYVAICHPILKMTLMSRVCWIMVATSWIIASLAIQHTWTWMLPCVSWEIRHLCE 180

PS Claim 1; Page 101; 182pp; English.

XX The invention relates to a method of representing sensory perception of
CC one or more odourants. The method comprises: (a) providing a
CC representative class of n olfactory receptors or ligand binding domains
CC (LBD) of these receptors; (b) measuring values X1 to Xn representative of
CC at least one activity of one or more odourants selected from: (i) binding
CC one or more odourants to the LBD of at least one of the n olfactory
CC receptors; (ii) activating at least one of the n olfactory receptors with
CC the one or more odourants; and (iii) blocking at least one of the n
CC olfactory receptors with the one or more odourants; and (c) generating a
CC representation of the sensory perception of odourants is useful for the
CC design and formulation of the sensory perception of odourants. AAUS5140-AAUS393
CC represent human olfactory G-coupled receptor amino acid sequences of the
XX invention

XX Sequence 316 AA;

Query Match 86.8%; Score 1390; DB 5; Length 316;
Best Local Similarity 87.0%; Pred. No. 1e-143;

Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MEIRNSTLGSGLVINGLINDSGSPDLATFTLLVMTALTSNGLLATITTEARLHPMY 60
DB 1 MEIRNSTLGSGLVINGLINDSGSPDLATFTLLVMTALTSNGLLATITTEARLHPMY 60
QY 61 LILGQSLMDLFTSVTPPALADFLRENTISFGGALOMFLATMGAEEDLLAFMAY 120
DB 61 LILGQSLMDLFTSVTPPALADFLRENTISFGGALOMFLATMGAEEDLLAFMAY 120
QY 121 DRYVAICHPKXTMTLSPRCWIMVATSWTSLASLAIIGHTMTMHLPCVSMERHDLCE 180
DB 121 DRYVAICHPKXTMTLSPRCWIMVATSWTSLASLAIIGHTMTMHLPCVSMERHDLCE 180
QY 181 IPPLKACADTSRYELIIVYGVTELLPISAVASYTLVFTVLRMPSNEBKKAALVT 240
DB 181 IPPLKACADTSRYELIIVYGVTELLPISAVASYTLVFTVLRMPSNEBKKAALVT 240
QY 241 CSNHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFTYITVPALNPLIYSLNKKEWMRA 300
DB 241 CSNHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFTYITVPALNPLIYSLNKKEWMRA 300
QY 301 LRRVLGKTYLLAHSTL 316
DB 301 LRRVLGKTYLLAHSTL 316

RESULT 13

ADC65823

ID ADC65823 standard; protein; 316 AA.

XX ADC65823;

XX 01-JAN-2004 (first entry)

DE Human GPCR protein SEQ ID NO:276.

KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
KM gene therapy.

XX Homo sapiens.

XX EP1270724-A2.

XX 02-JAN-2003.

XX 18-JUN-2002; 2002EP-00013517.

XX 18-JUN-2001; 2001JP-00246789.

XX (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX WPI; 2003-315783/31.
XX N-PSDB; ADC65822.

XX New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.

PS Claim 2; SEQ ID NO 276; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
CC sequences shown in ADC6549-ADC67617 represent GPCR's of the invention.

XX Sequence 316 AA;

Query Match 86.8%; Score 1390; DB 7; Length 316;
Best Local Similarity 87.0%; Pred. No. 1e-143;

Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MEIRNSTLGSGLVINGLINDSGSPDLATFTLLVMTALTSNGLLATITTEARLHPMY 60
DB 1 MEIRNSTLGSGLVINGLINDSGSPDLATFTLLVMTALTSNGLLATITTEARLHPMY 60
QY 61 LILGQSLMDLFTSVTPPALADFLRENTISFGGALOMFLATMGAEEDLLAFMAY 120
DB 61 LILGQSLMDLFTSVTPPALADFLRENTISFGGALOMFLATMGAEEDLLAFMAY 120
QY 121 DRYVAICHPKXTMTLSPRCWIMVATSWTSLASLAIIGHTMTMHLPCVSMERHDLCE 180
DB 121 DRYVAICHPKXTMTLSPRCWIMVATSWTSLASLAIIGHTMTMHLPCVSMERHDLCE 180
QY 181 IPPLKACADTSRYELIIVYGVTELLPISAVASYTLVFTVLRMPSNEBKKAALVT 240
DB 181 IPPLKACADTSRYELIIVYGVTELLPISAVASYTLVFTVLRMPSNEBKKAALVT 240
QY 241 CSNHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFTYITVPALNPLIYSLNKKEWMRA 300
DB 241 CSNHLIVGMFYGAATFMVLPSSFHSFKODNIIISVFTYITVPALNPLIYSLNKKEWMRA 300
QY 301 LRRVLGKTYLLAHSTL 316
DB 301 LRRVLGKTYLLAHSTL 316

RESULT 14

ABB81447

ID ABB81447 standard; protein; 317 AA.

XX ABB81447;

XX 28-AUG-2002 (first entry)

DE Human GPCR4b protein sequence SEQ ID NO:16.

KW Human; GPCR; G protein-coupled receptor; antihypertensive;
KM anorectic; antibacterial; fungicide; procoagulant; antiparkinsonian;
KM cytoskeletal; immunomodulator; metabolic; antidiabetic; anti-HIV;
KM hyperintensive; hypotensive; osteopathic; antiinflammatory; anti-HIV;
KM antiallergic; neuroprotective; antidiabetic; antidiabetic; antidiabetic;
KM antianemic; anticonvulsant; haemostatic; immunosuppressive; hepatotropic;
KM cerebroprotective; dermatological; antidiabetic; gynaecological; cancer;
KM nephroprotective; gene therapy; vaccine; developmental disorder; diabetes;
KM cardiomyopathy; atherosclerosis; neurodegenerative disorder;
KM autoimmune disorder; infectious disease; chromosome 1.

OS Homo sapiens.
 XX WO200226985-A2.
 XX
 XX 04-APR-2002.
 XX
 XX 28-SEP-2001; 2001WO-US030552.
 XX
 XX 28-SEP-2000; 2000US-0236284P.
 XX 28-SEP-2000; 2000US-0236286P.
 XX 03-OCT-2000; 2000US-0237581P.
 XX 06-OCT-2000; 2000US-0238735P.
 XX 16-OCT-2000; 2000US-0240736P.
 XX 05-JAN-2001; 2001US-0260019P.
 XX 08-JAN-2001; 2001US-026038P.
 XX 17-JAN-2001; 2001US-0262156P.
 XX 18-JAN-2001; 2001US-0262498P.
 XX 19-JAN-2001; 2001US-0263133P.
 XX 24-JAN-2001; 2001US-0263691P.
 XX 02-FEB-2001; 2001US-0266109P.
 XX 26-FEB-2001; 2001US-0271634P.
 XX 27-SEP-2001; 2001US-00965422.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Spytek KA, Casman S, Padigaru M, Dickson K, Vernet C,
 XX Spaderma SK, Shenoy S, Gerlach V, Ellerman K, Edinger S,
 XX McDougall JR, Smithson G, Li L, Malyankar UM, Taylor S, Gunther E,
 XX Tchernev VT;
 XX
 XX WPI: 2002-499866/53.
 XX N-PSDB; ABN89119.
 XX
 XX Novel G-protein coupled receptor polypeptides and nucleic acids for
 XX diagnosing, treating cardiomyopathy, atherosclerosis, cancer, and
 XX neurodegenerative, autoimmune disorders, infectious diseases and
 XX diabetes.
 XX
 XX Claim 1; Page 35; 213pp; English.
 XX
 XX ABN89112 to ABN89130 encoding the human G protein-coupled receptor
 XX (GPCR) proteins given in ABN81440 to ABN81458. GPCR proteins can have
 XX antiatherosclerotic, anorectic, antibacterial, fungicide, protozoacide,
 XX antiviral, analgesic, cyrostatic, immunomodulator, metabolic, hypotensive,
 XX antiaesthetic, antiparkinsonian, hypertensive, osteopathic, anti-HIV,
 XX antiinflammatory, antiinfectivity, neuroprotective, antianginal,
 XX cardiant, antulcer, antiallergic, nootropic, tranquiliser, neuroleptic,
 XX antidepressant, antiinfect, anticonvulsant, haemostatic, hepatotropic,
 XX immunosuppressive, cerebroprotective, dermatological, antiaddictive,
 XX neuropeptide and gynaecological activities, and can be used in vaccines
 XX and gene therapy. GPCR proteins and polynucleotides can be used for
 XX treating or preventing a GPCR-associated disorder such as
 XX cardiomyopathy, atherosclerosis, a disorder related to cell signal
 XX processing and metabolic pathway modulation, in a human. GPCR proteins
 XX and polynucleotides can also be used in the manufacture of a medicament
 XX for preventing or treating disorders or syndromes including developmental
 XX diseases, cardiomyopathy, atherosclerosis, cancer, neurodegenerative
 XX disorders, autoimmune disorders, infectious diseases and diabetes.
 XX ABN89131 to ABN89187 represent PCR primers and probes used in the
 XX exemplification of the present invention
 XX
 XX Sequence 317 AA;
 XX
 XX Query Match 52.4%; Score 839; DB 5; Length 317;
 XX Best Local Similarity 50.5%; Pred. No. 3e-83;
 XX Matches 156; Conservative 59; Mismatches 94; Indels 0; Gaps 0;
 XX
 XX 1 MELRNSTLSSGFTIVILNDSSGPELVATFTILYMLALTSNGLILATITEARLHPMY 60
 XX 1 MEQSNSTVAVADFLILFLSARFPLILFALILIVFTSTASNVMTILIHIDSRILTPMY 60
 XX 61 LILGQLSLMDLILFTSVTPKALADFLRRENTISFGCALQMLTALTMGSAEDILLAFMAY 120

DB 61 FLISQSLSDILIIYISTIVPKMLVDVQMSQRAISFACCTQHFLVYLTLAGAEFFELGLMSY 120
 QY 121 DRYVAICHPDKWTMTLSPRCWIMVATSWILASLIAIGHWTYTMHLPCFVSWELRLLEE 180
 DB 121 DRYVALCNLHPEDLMRSRKCMLIVAAWLGSDIDGFLILTPVTMPFPQASREINHPCE 180
 QY 181 IPEPLKACADTSRRRLIYYVGVTFLLPISAVASYTLVLTFTVLRMPSNEGRKALVT 240
 DB 181 VPALLKLSCTDTSAYETAMVCCIMMLLIPFVYSGSYRILITVYRMSABGRRAVAT 240
 QY 241 CSSHLIVGMFGAATFMYLPSFSPKQDNIIISVYTIIVPALNPLIYSLNKEVMRA 300
 DB 241 CSSHMVVSILFYANATVYLPHSHHTPPDQKAVSAFYTLTPTMLNPLIYSLNKDVTA 300
 QY 301 IRRVLGKYI 309
 DB 301 LQKVVRGV 309
 RESULT 15
 AAU24755
 ID AAU24755 standard; protein; 317 AA.
 XX
 XX AAU24755;
 XX
 XX 18-DEC-2001 (first entry)
 XX
 XX Human olfactory receptor A0LPR255.
 XX
 XX Human olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 XX Food additive; cosmetic; fragrance; pharmaceutical additive.
 XX
 XX Homo sapiens.
 XX
 XX WO200168805-A2.
 XX
 XX 20-SEP-2001.
 XX
 XX 13-MAR-2001; 2001WO-US007771.
 XX
 XX 13-MAR-2000; 2000US-0188914P.
 XX 24-MAR-2000; 2000US-0192033P.
 XX 12-APR-2000; 2000US-0198474P.
 XX 24-APR-2000; 2000US-0199335P.
 XX 26-MAY-2000; 2000US-0207702P.
 XX 23-JUN-2000; 2000US-0213849P.
 XX 16-AUG-2000; 2000US-0226534P.
 XX 07-SEP-2000; 2000US-0230733P.
 XX 07-FEB-2001; 2001US-0266862P.
 XX
 XX (SENO-) SENOMYX INC.
 XX
 XX Zozulya S;
 XX
 XX WPI: 2001-570867/64.
 XX N-PSDB; AAS42448.
 XX
 XX Nucleic acids encoding human olfactory G protein-coupled receptors,
 XX useful for screening for compounds involved in olfactory sensation, where
 XX the compounds can be used in the food, pharmaceutical and cosmetic
 XX industries to customize odors.
 XX
 XX Claim 60; Page 191; 319pp; English.
 XX
 XX The invention relates to nucleic acids encoding human olfactory
 XX receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 XX specifically recognize molecules, odourants, that elicit specific
 XX olfactory sensation. The human olfactory receptors and polynucleotides
 XX encoding them are useful for screening a library of chemical compounds
 XX for compounds that are involved in olfactory sensation. Modulators of
 XX their activity are useful for pharmacological and genetic modulation of
 XX olfactory signalling pathways. Therefore, they can be used in the food,
 XX pharmaceutical and cosmetic industries to customise odours and

CC fragrances. The present sequence is a human olfactory receptor of the
CC invention
XX
SQ Sequence 317 AA;

Query Match 52.0%; Score 833; DB 4; Length 317;
Best Local Similarity 50.5%; Pred. No. 1.4e-82;
Matches 156; Conservative 57; Mismatches 96; Indels 0; Gaps 0;

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QY 1 MELRNSTLIGSGFIIIVGILINDSGPELVATFTILYMLALTSNGLLLATITTEARLHMPY 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 MEQSNYSVYADFIILGLFSNARFPWLLFALILVFLTSIASNVVKIILIHIDSRHLPY 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 61 LLLGQLSIMDLFTSVVTPKALADFIKRENTISFGGALQMFALITMGSAEDLLAFMAY 120
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 61 FLLSQLSIRDLIVSTIVPKMLVDQVMSQRAISFAGCTAOHFILYLTLAGAEFFLLGLMSY 120
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 121 DRYVAICHPLKYMTLMSPRVCMIMWATSWILASLIAIHTWYTMHLPCVSWETRHLC 180
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 121 DRYVAICNPLHYPLMSRKICMLIVAAWLGSGIDGFLTPVTMQPFCAAREINHFCE 180
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 181 IPELKLACADTSRELIIVYTGVTLLPISALVASYTLVLFVTLMPSNEGKKAIVT 240
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 181 VPALLKLSCTDTSAYETAMVCCIMMLIFPSVISGSYTRILITVYMSSEABGKKAIVT 240
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 241 CSSHLIYVMFYGAATPMYVLPSSFHSPKODNIIISVYTTVTPALNPLIYSLRNKEVMA 300
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 241 CSSHMVYVSLFYGLAMTYTVLPHSYHTPEODKAVSAFYTLITPMLNPLIYSLRNKDVTA 300
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 301 LRRVLGKYI 309
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 301 LQKVGRGV 309
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

Search completed: August 18, 2004, 08:56:44
Job time : 96 secs

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RESULT 2

A46247

Olfactory receptor OR3 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999

C:Accession: A46247

R:Ref, P.: Hermans-Borgmeyer, I.; Arterios-Pln, H.; Beasley, L.; Dionne, V.E.; Heinemann

Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992

A:Title: Spatial pattern of receptor expression in the olfactory epithelium.

A:Reference number: A46247; MUID:93028384; PMID:11384038

A:Accession: A46247

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-312 <NEF>

A:Cross-references: GB:M84005; NID:g200153; PIDN:AAA39862.1; PID:g200154

A:Note: sequence extracted from NCBI backbone (NCBI:115362)

C:Superfamily: olfactory receptor OR14

Query Match 42.7%; Score 684; DB 2; Length 312;

Best Local Similarity 42.3%; Pred. No. 7.5e-51;

Matches 130; Conservative 68; Mismatches 109; Indels 0; Gaps 0;

QY 1 MELNSTLGGSGFLIVGILNDGSPDLVATFTIIMLALTSNGLLALITTEARLHPMY 60

Db 1 MEVDNSSSGFLIVGSDHPELHIFFAVILASVLTLLVGNLTITILSLRDLARLHPMY 60

QY 61 LLLGQLSLMDL-LFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLAFMAY 120

Db 61 FFLNLSLDAFTSSVPMKLMGPDKITSYGGCTQLVFLMGAECILLVMAF 120

QY 121 DRYVAICHPKXMTLSPVCMIVATSWILASLAIIGHTMYTMLPFCVSWETRLHCE 180

Db 121 DRYVAICHPKXMTLSPVCMIVATSWILASLAIIGHTMYTMLPFCVSWETRLHCE 180

QY 121 DRYVAICHPKXMTLSPVCMIVATSWILASLAIIGHTMYTMLPFCVSWETRLHCE 180

Db 121 DRYVAICHPKXMTLSPVCMIVATSWILASLAIIGHTMYTMLPFCVSWETRLHCE 180

QY 181 IPPLLKLAADTSRYELIIVTGTFLPLIPSAIVASTLVLFVLRMPSNEGRKALVT 240

Db 181 VPAIKLACGDTSLNEAVGVCFFETVVPVSVILVSCYFLAQVMTKRSVEGRKAFNT 240

QY 241 CSSHLIVGMFYGAATFMYLPSSFHSPKQNIISVFITITPLNPLIYSLRKWEVRA 300

Db 241 CVSHLVVFLFYGSAIVGLLPAKSSNQSGKFTSLFYSVVTVMVPLIYTLRNEKVGCA 300

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

Db 301 LRRVLGK 307

QY 301 LRRVLGK 307

C:Keywords: olfaction; taste bud; transmembrane protein
 F:24-47/Domain: transmembrane #status predicted <TM1>
 F:56-77/Domain: transmembrane #status predicted <TM2>
 F:99-118/Domain: transmembrane #status predicted <TM3>
 F:138-162/Domain: transmembrane #status predicted <TM4>
 F:195-217/Domain: transmembrane #status predicted <TM5>
 F:236-258/Domain: transmembrane #status predicted <TM6>
 F:271-291/Domain: transmembrane #status predicted <TM7>

Query Match 41.9%; Score 672; DB 2; Length 311;

Best Local Similarity 44.6%; Pred. No. 7.9e-50;

Matches 140; Conservative 56; Mismatches 110; Indels 8; Gaps 4;

QY 3 LNSTLGGSGFLIVGILNDGSPDLVATFTIIMLALTSNGLLALITTEARLHPMY 59

Db 1 MEVDNSSSGFLIVGSDHPELHIFFAVILASVLTLLVGNLTITILSLRDLARLHPMY 57

QY 60 YLLGQLSLMDL-LFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLAFM 118

Db 58 YFLANLSPADMGILISVT-KMLENVOTGCHTISYGCITOMYLFMMFDDLSFLAVM 116

QY 119 AYDRYVAICHPKXMTLSPVCMIVATSWILASLAIIGHTMYTMLPFCVSWETRLHCE 178

Db 117 AYDRYVAICHPKXMTLSPVCMIVATSWILASLAIIGHTMYTMLPFCVSWETRLHCE 176

QY 179 CEIPPLKLAADTSRYELIIVTGTFLPLIPSAIVASTLVLFVLRMPSNEGRKAL 238

Db 177 CDVTSVMKSCSDPHVVELVLSGFGTVMVFPFSAIVSYHIVFAVARIQSGSSKAF 236

QY 239 VTGSHLIVGMFYGAATFMYLPSSFHSPKQNIISVFITITPLNPLIYSLRKWEV 298

Db 237 STGSHLIVGMFYGAATFMYLPSSFHSPKQNIISVFITITPLNPLIYSLRKWEV 296

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

Db 297 GALKRLSHRRILS 310

QY 299 RALRRVLGKYLTA 312

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Db      59 PMYFELSLSPVDLCYSTVITPKMLVNFGLKGNKITTSCEMAQGFPAIFVTTCYLLTV 118
QY      118 MAYRYVALCHPLKMTLMSPRVCMVAVSWILASILAIGHTMYTMEPCVSWEIRHL 177
Db      119 MAYDRYVALCRPFLYNYMISRLCSLLVAVFSLGFSVAHVHTSAMNLSCKSYLISHY 178
QY      178 LCEIPFLKACADTSREYLLIYVGTFTLLPISAVASTLVLFVLRMPSEGRKKA 237
Db      179 FCDMLPLKACSWTHLNEILLITIGLINTVPLIAVAISVFLICSLIRSRSEGRSKA 238
QY      238 LVTCSHLLVGMFGAATFMVYLPSSFSHPKODNIISVFYITVTPALNPLIYSRKVEY 297
Db      239 FGCCSHLLMVGIFFGSITTMYLKRPSSNSLDEKSVSVETTYITVPLNPLIYSLRKVDV 298
QY      298 MRALRR 303
Db      299 KKALGR 304

```

RESULT 5

olfactory receptor - dog
 C/Species: Canis lupus familiaris (dog)
 C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 26-Aug-1999
 C/Accession: S20571
 R/Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.; Nature 355, 453-455, 1992
 A/Title: Expression of members of the putative olfactory receptor gene family in mammal
 A/Reference number: S20571, MUID:9213132; PMID:1370859
 A/Accession: S20571
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-313 <PAR>
 A/Cross-references: EMBL:X64996; NID:9890; PIDN:CAA46129.1; PID:9891
 C/Suprafamily: olfactory receptor OR14
 C/Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match      41.7%; Score 668.5; DB 2; Length 313;
Best Local Similarity 42.6%; Pred. No. 1.6e-49;
Matches 130; Conservative 60; Mismatches 114; Indels 1; Gaps 1;

QY      1 MELRNTLGSGLVINGLINDSGSPPELLYATFTLLMALTNSGLLALTTEARLHPMY 60
Db      1 MTEKNTVSEFVLGLGPIPDQDRLFYALFLAMYVTLTGLNLLITVLQLDSHLTPMY 60
QY      61 LLLGQLSLMDLFTSVVTPKALADFLRRENTISFGGCAQMFALTMGSABDLILAFMY 120
Db      61 LFLSNLSFSDLCSSVTMPKRLQNMGSQVPSIPYACLTQMYFLLFGDLSEFLVAMAY 120
QY      121 DRVVAICHPKMTLMSPRVCMVAVSWILASILAIGHTMYTMEPCVSWEIRHLCE 180
Db      121 DRVVAICHPFLHYTTIMSPKLSLAVSWLTFMFHVAHTLLMARLCFCAN-TIPFED 179
QY      181 IPEPLKACADTSREYLLIYVGTFTLLPISAVASTLVLFVLRMPSEGRKKA 240
Db      180 MSALTKLACSDTQVNELVLFIMGGLILVLPFLIITISYARIYSILKVSAGICGVFST 239
QY      241 CSSHLLVGMFGAATFMVYLPSSFSHPKODNIISVFYITVTPALNPLIYSRKVEYMA 300
Db      240 CGSHLSVSLFYGTVIGLYLCSANNSTYKETIMAMTYVTPMLNPLIYSLRKDKMCA 299
QY      301 LRRVL 305
Db      300 LRRVI 304

```

RESULT 6

olfactory receptor Part1 - human
 C/Species: Homo sapiens (man)
 C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 26-Aug-1999
 C/Accession: A57069

R/Fan, W.; Liu, Y.C.; Parimoo, S.; Weissman, S.M.
 Genomics 27, 119-123, 1995
 A/Title: Olfactory receptor-like genes are located in the human major histocompatibility
 A/Reference number: A57069; MUID:95394447; PMID:7665158
 A/Accession: A57069
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-316 <FAN>
 A/Cross-references: GB:L35475; NID:g1041044; PIDN:AA836567.1; PID:g601919
 C/Genetics:
 A/Gene: GDB:FAT11; OLF2
 A/Cross-references: GDB:L323249; OMIM:600578
 A/Map position: 6p21.3-6p21.3
 C/Suprafamily: olfactory receptor OR14

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Query Match      41.1%; Score 659; DB 2; Length 316;
Best Local Similarity 40.1%; Pred. No. 1e-48;
Matches 123; Conservative 72; Mismatches 110; Indels 2; Gaps 1;

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QY      1 MELRNTLGSGLVINGLINDSGSPPELLYATFTLLMALTNSGLLALTTEARLHPMY 60
Db      1 MDNQST--PGFLLGSEHPIGRITLVVITISYLLTVGNLTLLIISLMDTKLSPMY 58
QY      61 LLLGQLSLMDLFTSVVTPKALADFLRRENTISFGGCAQMFALTMGSABDLILAFMY 120
Db      59 FFLSNLSFSDLCFTSCVPMQLNLMGPCKTISFLDCSVQIFLISGTEICILMKVMAF 118
QY      121 DRVVAICHPKMTLMSPRVCMVAVSWILASILAIGHTMYTMEPCVSWEIRHLCE 180
Db      119 DRVVAICHPFLHYTTIMSPKLSLAVSWLTFMFHVAHTLLMARLCFCAN-TIPFED 178
QY      181 IPEPLKACADTSREYLLIYVGTFTLLPISAVASTLVLFVLRMPSEGRKKA 240
Db      179 VPALIRLSCEDSYNLIQVAVSVFLVPLSLIYSYGAILTAVLRINSATMKRAFGT 238
QY      241 CSSHLLVGMFGAATFMVYLPSSFSHPKODNIISVFYITVTPALNPLIYSRKVEYMA 300
Db      239 CGSHLLVVTLLFYSSVIAVLQPNPYAQGRKFGFLVAVGTPSLNPLVYTLANKKIRA 298
QY      301 LRRVLGK 307
Db      299 LRRLLGK 305

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RESULT 7

olfactory factor OR37 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
 C/Accession: S29711
 R/Fanning, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubic, S.; Baumtark, C.; Breer
 Nature 361, 353-356, 1993
 A/Title: Cloning and expression of odorant receptors.
 A/Reference number: S29707; MUID:93149273; PMID:7678922
 A/Accession: S29711
 A/Molecule type: mRNA
 A/Residues: 1-305 <RAM>
 C/Suprafamily: olfactory receptor OR14

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Query Match      40.9%; Score 655.5; DB 2; Length 305;
Best Local Similarity 44.0%; Pred. No. 2e-48;
Matches 136; Conservative 54; Mismatches 102; Indels 17; Gaps 6;

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```

QY      13 ILVGLINDSGSP--ELVATFT--IIMYALTNSGLLALTTEARLHPMYLLGQLSM 69
Db      1 LLLGL--SGPKTILYFVIVLVYHTNGVLLIASIPDSHLTPMYEPFLNLSFL 57
QY      70 DLLFTSVTPKALADFLRRENTISFGGCAQMFALTMGSABDLILAFMYARYVAICHP 129
Db      58 DICYTSSVPTSLVSLIKKNISFGCTGVQMFVGFANSGTECLLGMMAFRRYVAICNP 117
QY      130 LKMTLMSPRVCMVAVSWILASILAIGHTMYTMEPCVSWEIRHLCEIPLKAC 189

```

Db 118 LRYSVMSKEVYVSMASWFSGGINSVQTSIAMLRLPCGNVYNHFTCEVLAVLKAC 177
 QY 190 ADFSRRELIIVTGVTFLLPISAIYASITLVLPVLRMSNGRKAALVTCSSHLIVG 249
 Db 178 ADISLNVTVVIVSNMFLVPLLIIFPSYVLIYTLIRNNSASGRRAFASTCSAHLTVV 237
 QY 250 MFGAATFMYVLPSS-----FHSRKQDNISVFYITVTPALNPLIYSIRNKEVRAAL 301
 Db 238 IFPGTISMAKPSQDLTKDKRQGT--SDKIISLFGVTVTPMLNPIIYSIRNNDVAAV 295
 QY 302 RRVL-GKXI 309
 Db 296 KYIIKKXI 304

RESULT 8
 A37286
 Olfactory receptor 115 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C:Accession: A37286
 R:Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A:Reference number: A23701; MUID:91191556; PMID:1840504
 A:Accession: A37286
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-314 <RBC>
 A:Cross-references: GB:M64392; NID:g205845; PIDN:AAA4175.1; PID:g205846
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 40.4%; Score 648; DB 2; Length 314;
 Best Local Similarity 41.7%; Pred. No. 8.8e-48;
 Matches 128; Conservative 59; Mismatches 120; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIVGLINDSGSPFLYATFTIYMLALTSNGLLAITTEARLHMPY 60
 Db 1 MTERNQTVISQFLGLPPEHQHVYALFLSMYTLTGLNLIILILDSHLHTPMY 60
 QY 61 LILGQLSIMDLFTSVTPKALADFLRENTISFGCALQMFALTWGSABDLIAFMAY 120
 Db 61 LFLNLSFSDLCFSSVTMPKILQNMQSVPSIPFAGCLTQLYFYLVFADLESFLLVAMAY 120
 QY 121 DRYVAICHPKMYTMSPRVCWIMVATSWILASIALIGHYTMHLPCVSWERHLLCE 180
 Db 121 DRYVAICHPKMYTMSPRVCWIMVATSWILASIALIGHYTMHLPCVSWERHLLCE 180
 QY 121 DRYVAICHPKMYTMSPRVCWIMVATSWILASIALIGHYTMHLPCVSWERHLLCE 180
 Db 121 DRYVAICHPKMYTMSPRVCWIMVATSWILASIALIGHYTMHLPCVSWERHLLCE 180
 QY 181 IPLLKLIACDTSRELIIVTGVTFLLPISAIYASITLVLPVLRMSNGRKAALVT 240
 Db 181 IPLLKLIACDTSRELIIVTGVTFLLPISAIYASITLVLPVLRMSNGRKAALVT 240
 QY 241 CGSHLSVSLFYGITIGIYLCPSANNSVYKETVAMMTVTPMLNPIIYSIRNNDMEA 300
 Db 241 CGSHLSVSLFYGITIGIYLCPSANNSVYKETVAMMTVTPMLNPIIYSIRNNDMEA 300
 QY 301 LRRVLGK 307
 Db 301 LRRVLGK 307
 QY 301 LRRVLGK 307
 Db 301 LRRVLGK 307

RESULT 9
 S29707
 Olfactory receptor OR5 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
 C:Accession: S29707; B37286
 R:Raming, K.; Krieger, J.; Strotmann, J.; Boehhoff, I.; Kubick, S.; Baumstark, C.; Breez
 Nature 361, 353-356, 1993
 A:Title: Cloning and expression of odorant receptors.
 A:Reference number: S29707; MUID:93149273; PMID:7678922
 A:Accession: S29707

A:Molecule type: mRNA
 A:Residues: 1-314 <RAM>
 R:Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A:Reference number: A23701; MUID:91191556; PMID:1840504
 A:Accession: B37286
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 193-236 <RBC>
 A:Cross-references: GB:M64375; NID:g205811; PIDN:AAA41738.1; PID:g205812
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; membrane protein

Query Match 40.2%; Score 644; DB 2; Length 314;
 Best Local Similarity 40.4%; Pred. No. 1.9e-47;
 Matches 124; Conservative 66; Mismatches 117; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIVGLINDSGSPFLYATFTIYMLALTSNGLLAITTEARLHMPY 60
 Db 1 MTERNQTVISQFLGLPPEHQHVYALFLSMYTLTGLNLIILILDSHLHTPMY 60
 QY 61 LILGQLSIMDLFTSVTPKALADFLRENTISFGCALQMFALTWGSABDLIAFMAY 120
 Db 61 LFLNLSFSDLCFSSVTMPKILQNMQSVPSIPFAGCLTQLYFYLVFADLESFLLVAMAY 120
 QY 121 DRYVAICHPKMYTMSPRVCWIMVATSWILASIALIGHYTMHLPCVSWERHLLCE 180
 Db 121 DRYVAICHPKMYTMSPRVCWIMVATSWILASIALIGHYTMHLPCVSWERHLLCE 180
 QY 181 IPLLKLIACDTSRELIIVTGVTFLLPISAIYASITLVLPVLRMSNGRKAALVT 240
 Db 181 IPLLKLIACDTSRELIIVTGVTFLLPISAIYASITLVLPVLRMSNGRKAALVT 240
 QY 241 CGSHLSVSLFYGITIGIYLCPSANNSVYKETVAMMTVTPMLNPIIYSIRNNDMEA 300
 Db 241 CGSHLSVSLFYGITIGIYLCPSANNSVYKETVAMMTVTPMLNPIIYSIRNNDMEA 300
 QY 301 LRRVLGK 307
 Db 301 LRRVLGK 307

RESULT 10
 H23701
 Olfactory receptor 19 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C:Accession: H23701
 R:Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A:Reference number: A23701; MUID:91191556; PMID:1840504
 A:Accession: H23701
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-314 <RBC>
 A:Cross-references: GB:M64388; NID:g205837; PIDN:AAA41751.1; PID:g205838
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 40.0%; Score 641; DB 2; Length 314;
 Best Local Similarity 40.4%; Pred. No. 3.5e-47;
 Matches 124; Conservative 62; Mismatches 121; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIVGLINDSGSPFLYATFTIYMLALTSNGLLAITTEARLHMPY 60
 Db 1 MTERNQTVISQFLGLPPEHQHVYALFLSMYTLTGLNLIILILDSHLHTPMY 60
 QY 61 LILGQLSIMDLFTSVTPKALADFLRENTISFGCALQMFALTWGSABDLIAFMAY 120
 Db 61 LFLNLSFSDLCFSSVTMPKILQNMQSVPSIPFAGCLTQLYFYLVFADLESFLLVAMAY 120

Query Match

Best Local Similarity 40.0%; Score 640; DB 2; Length 304;
Matches 130; Conservative 53; Mismatches 116; Indels 0; Gaps 0;

Query 12 FLVGLNDGSGPELLYATFTILYMLALTSNGLLLALITLARLHMPYLLIGQLSMDL 71
Db 5 FLIAGLTDPGGLMPLFLEFLGFYMTVGNLIGLFLGLNSHLTPMYFFLEFLNSVDF 64

Query 72 LFTSVTPKRALDPLRENTISFGCALQWFLALTMGSAEDLLAFMAYDRVATCHPLK 131
Db 65 CFSSTIIPMLMSFISKNIISHSGCMTQLFFCPFVSVETFTLSAMAYDRVATCNPLM 124

Query 132 YMTLSPRYCWMVATSWMLIASLLAIGHWTYTMHLPEFCVSEIRHLCEIPLKLACAD 191
Db 125 YVTWSPQVCLLLDGLAYVWGFSAMAHGTGMLMLTPADLVNHPMCDILPILBELSCNS 184

Query 192 TSYRELIIVYGVTFLLPLIPSAIVASYTLVLFVLRMPSNEGRKKALVTCSSHLIVGME 251
Db 185 FEINELIVPIVAVIDIAVPIVSIYSALILSLIRHMTSGRSKAFSTCSSHLIVCLL 244

Query 252 YGAATFMVYLPSFSFHSKQONIIISVFETIYTPALNPLIYSLRNKEVMAALRRVGLKYL 310
Db 245 FEGSAGFMVYLPILPLDQGVSSLFYTIIVFEMNPLIYSLRNKKVVALRRTLGKTIIL 303

RESULT 12

olfactory receptor I3 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C:Accession: E23701
R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701; MUID:91191556; PMID:1840504
A:Accession: E23701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-310 <auc>
C:Superfamily: Olfactory receptor OR14

Query 121 DRYVAICHELKXWTLMSPRCWMVATSWLASLLAIGHWTYTMHLPEFCVSEIRHLCE 180
Db 121 DRYVAICHELKXWTLMSPRCWMVATSWLASLLAIGHWTYTMHLPEFCVSEIRHLCE 180

Query 181 IEPPLKLACADTSRYEHLIIVYGVTFLLPLIPSAIVASYTLVLFVLRMPSNEGRKKALVT 240
Db 181 METLKLKACSDTHDNEALFILGGPIYVLPFLLIIVSARVYSSIFKYPSSGSIHKAPST 240

Query 241 GSHLIVGMEFYGAATFMVYLPSFSFHSKQONIIISVFETIYTPALNPLIYSLRNKEVMA 300
Db 241 GSHLIVGMEFYGAATFMVYLPSFSFHSKQONIIISVFETIYTPALNPLIYSLRNKEVMA 300

Query 301 LRRVLGK 307
Db 301 LRRVLGK 307

RESULT 11

olfactory receptor OR14 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C:Accession: S29709
P:Raming, K.; Krieger, J.; Strothmann, J.; Boekhoff, I.; Kubic, S.; Baumstark, C.; Bree
A:Title: Cloning and expression of odorant receptors.
A:Reference number: S29707; MUID:93149273; PMID:7678922
A:Accession: S29709
A:Molecule type: mRNA
A:Residues: 1-304 <RAM>
C:Superfamily: olfactory receptor OR14

```

C:Keywords: G protein-coupled receptor; transmembrane protein
Query Match      39.6%; Score 634; DB 2; Length 310;
Best Local Similarity 38.9%; Pred. No. 1.3e-46;
Matches 118; Conservative 69; Mismatches 116; Indels 0; Gaps 0;

OY 3 LRNSTLGGFLIVGLINDSGPELLYATFTLLYMLALTSNGLLLAITTEARLHMPYLL 62
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MNNQTFITQFLGLGLPIPEEHQHLFYALFLVMYLLTLLGNLLIIVLVDLSQHLTPMYLF 60

OY 63 LGSLLMDLPTSVMTPKALADFLRRENTISFGCALQMFALTMGSAEDLLAFMAADR 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 LSNLSFSDLCFSSVTMPFLQNMESQDTSIYGGALQTYFPFMFGDMESTLVAMAADR 120

OY 123 YVAICPLKTYMTLMSPRVCWIMVATSWMLASLLAIGHMYTMHLPCFVSWEIRHLCEIP 182
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 YVAICPLKTYMTLMSPRVCWIMVATSWMLASLLAIGHMYTMHLPCFVSWEIRHLCEIP 180

OY 183 PLKLACADTSRYELIIVTGVTFLLPISAIIVASYTLVFTVLRMPSNEGRKALVTCS 242
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 VLLKLACSDTYINELMIFIMSTLLIIPFLIIVMSYARIISILKVPSTQICXVFCG 240

OY 243 SHLIYVGMFYGAATFMVVLPSFHSFKODNIISVFYITVPAALPLYSLRNKEVMRLR 302
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 SHLSVSLSEFTYITGLYLCFAGNNSYVKEWMAAMTYVTPLMEFTYSLRNKDMKRALI 300

OY 303 RVL 305
    ||
DB 301 RVI 303

RESULT 13
S20572
Olfactory receptor - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
C:Accession: S20572
R:Parmentier, M.; Libert, F.; Schumans, S.; Schiffmann, S.; Lefort, A.; Esgerickx, D.;
Nature 355, 453-455, 1992
A:Title: Expression of members of the putative olfactory receptor gene family in mammal
A:Reference numbers: S20571; MUID:92131132; PMID:1370859
A:Accession: S20572
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-314 <PAR>
A:Cross-references: EMBL:X64994; NID:G32085; PIDN:CAA46127.1; PID:G32086
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      39.5%; Score 632; DB 2; Length 314;
Best Local Similarity 41.4%; Pred. No. 2e-46;
Matches 125; Conservative 57; Mismatches 120; Indels 0; Gaps 0;

OY 4 RNSTLGGFLIVGLINDSGPELLYATFTLLYMLALTSNGLLLAITTEARLHMPYLL 63
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 QNQTISISFLLGLPIQPEQNLCYALFLYMLTLLGNLLIIVLRIDSHLTPMYLFL 63

OY 64 GQLSMDLPTSVMTPKALADFLRRENTISFGCALQMFALTMGSAEDLLAFMAADR 123
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 SNLSFSDLCFSSVTMPFLQNMESQDTSIYGGALQTYFPFMFGDMESTLVAMAADR 123

OY 124 YVAICPLKTYMTLMSPRVCWIMVATSWMLASLLAIGHMYTMHLPCFVSWEIRHLCEIP 183
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 YVAICPLKTYMTLMSPRVCWIMVATSWMLASLLAIGHMYTMHLPCFVSWEIRHLCEIP 183

OY 184 LKLACADTSRYELIIVTGVTFLLPISAIIVASYTLVFTVLRMPSNEGRKALVTCS 243
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 LKLAFSTPRNENWIFIMGIIIVIPLLILGYSYARIVSSILKVPSTQICXVFCG 243

OY 244 HLIYVGMFYGAATFMVVLPSFHSFKODNIISVFYITVPAALPLYSLRNKEVMRLR 303
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 244 HLSVSLSEFTYITGLYLCFAGNNSYVKEWMAAMTYVTPLMEFTYSLRNKDMKRALR 303

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QY 304 VL 305
Db 304 VI 305

RESULT 14

olfactory receptor F5 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C/Accession: B23701
R/Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A/Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A/Reference number: A23701; MUID:91191556; PMID:1840504
A/Accession: B23701
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-313 <BUC>
A/Cross-references: GB:M64377
C/Superfamily: olfactory receptor OR14
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 38.8%; Score 622; DB 2; Length 313;
Best Local Similarity 40.3%; Pred. No. 1.4e-45;
Matches 123; Conservative 55; Mismatches 127; Indels 0; Gaps 0;

QY 1 MELNSTGSGFIIVGILNDGSPPELLYATFTIYMLATNSGILLATITTEARLHMPY 60
Db 1 MSTNQSVTFELTGLSRPQQQLFLFLIMLATVGLNLIILAIIGTDSRLHTPMY 60
QY 61 LLLGQLSLMDLFTSVVTPKALADFLRENTISFGGALQMFALITWGSADLLIAFMAY 120
Db 61 FFLNLSPFDVCFSSSTVPKLANHILGSCAISFGGCTQLYFLAVGNMDFLLAVMSY 120
QY 121 DRYVAICHPLKMYTLMSEPRVWIVATSWIIASLAIIGHTMYTWHLPVCVSWIRHLICE 180
Db 121 DRFAVAICHPLHTTKMRQLCVLLVGSVWVANNCILHILMARKSCADNMIPHEFCD 180
QY 181 IPLLKLACADTSRYELIIVTGVTFLLPISATVASYTLVLFVLRMPNSGRRKALVT 240
Db 181 GTPILKISCSITHNELMILTEGAVWVTPVLCILISITHITCAVLKRVSSPRGKSFST 240
QY 241 CSHLIIVGMFYGATFMYVLPSSPFSKQDNIIISVFTIYTPALNPLIYSLRNKEVWRA 300
Db 241 CGSHLAVVCLFYGIVIAVYFNPSSSHLAGRDMAAAVMYAVVTPMLNPIYSLRNSDKAA 300
QY 301 LRRVL 305
Db 301 LRRVL 305

RESULT 15

olfactory receptor 114 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C/Accession: 123701
R/Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A/Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A/Reference number: A23701; MUID:91191556; PMID:1840504
A/Accession: 123701
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-312 <BUC>
A/Cross-references: GB:M64391; NID:g205843; PIDN:AAA41754.1; PID:g205844
C/Superfamily: olfactory receptor OR14
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 38.8%; Score 621; DB 2; Length 312;
Best Local Similarity 41.5%; Pred. No. 1.7e-45;
Matches 125; Conservative 55; Mismatches 121; Indels 0; Gaps 0;

QY 5 NSTIGSGFIIVGILNDGSPPELLYATFTIYMLATNSGILLATITTEARLHMPY 64
Db 5 NQTLILFELLGLPIPEYHLLFYALFLANVLTIIIGNLLIIVLRDSHLHMMYFLS 64
QY 65 QLSIMDLFTSVVTPKALADFLRENTISFGGALQMFALITWGSADLLIAFMAYDRYV 124
Db 65 NLSFSDLCFSSVTPKLLQNMQSVPSISYTGCTQLYFVWFEGDMESFLIYVNAAYDRYV 124
QY 125 AICPLKMYTLMSEPRVWIVATSWIIASLAIIGHTMYTWHLPVCVSWIRHLICEPPL 184
Db 125 AICPLKMYTLMSEPRVWIVATSWIIASLAIIGHTMYTWHLPVCVSWIRHLICEPPL 184
QY 185 LKLAACADTSRYELIIVTGVTFLLPISATVASYTLVLFVLRMPNSGRRKALVTCSH 244
Db 185 LKLSGSDIYVNEMLIYILGIIIIIPLLIYMSYVRIFFSILKFPSTQDIYKVFSTGSH 244
QY 245 LIIVGMFYGATFMYVLPSSPFSKQDNIIISVFTIYTPALNPLIYSLRNKEVWRA 304
Db 245 LSVTLFYGITFGIYLCPSGNNSTVKEIAMAMMYTAVTPMLNPIYSLRNSDKA 304
QY 305 L 305
Db 305 I 305

Search completed: August 18, 2004, 08:59:04
Job time : 17 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 08:34:28 ; Search time 13 Seconds

(without alignment)
1265.705 Million cell updates/sec

Title: US-10-024-444B-2

Sequence: 1 MEIRNSTGSGFTLVGILND.....VRAALRVLGKTLIAHSTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1390	86.8	316	1 O2AG_HUMAN	Q9h205 homo sapien
2	825	51.5	311	1 O2T1_HUMAN	Q4369 homo sapien
3	816	50.9	314	1 O221_HUMAN	Q8ng97 homo sapien
4	811	50.6	323	1 O2T2_HUMAN	Q8ngx2 homo sapien
5	804	50.2	315	1 O2T5_HUMAN	Q8nh02 homo sapien
6	801	50.0	316	1 O2T8_HUMAN	Q8nh01 homo sapien
7	794	49.6	312	1 O2M6_HUMAN	Q8ng83 homo sapien
8	793	49.5	320	1 O2AK_HUMAN	Q8ng84 homo sapien
9	777	48.5	312	1 O2M7_HUMAN	Q8ng81 homo sapien
10	776	48.4	320	1 O2T4_HUMAN	Q8nh03 homo sapien
11	749	46.8	313	1 O2T3_HUMAN	Q8nh00 homo sapien
12	747.5	46.7	312	1 O2L8_HUMAN	Q8nh09 homo sapien
13	733.5	45.8	312	1 O2L2_HUMAN	Q8nh16 homo sapien
14	721	45.0	310	1 O2A1_HUMAN	Q8ngt5 homo sapien
15	713.5	44.5	312	1 O2L8_HUMAN	Q8ng80 homo sapien
16	708.5	44.2	312	1 O2L2_HUMAN	Q8ng49 homo sapien
17	702	43.8	314	1 O2D3_HUMAN	Q8ng83 homo sapien
18	696	43.4	315	1 O2V2_HUMAN	Q8ng30 homo sapien
19	695	43.4	315	1 O2V3_HUMAN	Q8ngv1 homo sapien
20	688	42.9	310	1 O2AC_HUMAN	Q8ngt7 homo sapien
21	684.5	42.7	323	1 O2AE_HUMAN	Q8nh44 homo sapien
22	684	42.7	312	1 O2L1_MOUSE	Q8ng375 mus musculu
23	679	42.4	314	1 O2L1_MOUSE	Q8ng375 mus musculu
24	678	42.3	312	1 O2H2_HUMAN	Q8ngv9 mus musculu
25	678	42.3	314	1 O2D1_HUMAN	Q8ngv5 homo sapien
26	677.5	42.3	316	1 O2K2_HUMAN	Q8ngt1 homo sapien
27	676	42.2	316	1 O2H3_HUMAN	Q15062 homo sapien
28	675	42.1	312	1 O2A1_HUMAN	Q8ng84 homo sapien
29	674	42.1	313	1 O2G1_PANTR	Q8ngt9 pan troglod
30	671.5	41.9	309	1 O2G3_HUMAN	Q8ngx4 homo sapien
31	671	41.9	318	1 O2C2_HUMAN	Q8ngs9 homo sapien
32	668.5	41.7	313	1 O2F2_CANFA	P30955 canis faml
33	667	41.6	316	1 O2H1_HUMAN	Q9gzk4 homo sapien

34	666.5	41.6	319	1 O2S2_HUMAN	Q8ngt1 homo sapien
35	666	41.6	311	1 O1N3_HUMAN	Q8ng50 homo sapien
36	664	41.4	317	1 O2C3_HUMAN	Q8ngs6 homo sapien
37	663	41.4	317	1 O2C4_MOUSE	Q8vfk7 mus musculu
38	663	41.4	318	1 O2C4_MOUSE	Q8ngs5 homo sapien
39	663	41.4	324	1 O2R7_MOUSE	Q8v8s2 mus musculu
40	662.5	41.4	311	1 O1I6_HUMAN	Q8ngt2 homo sapien
41	662	41.3	309	1 O1A1_HUMAN	Q8ngt2 homo sapien
42	662	41.3	317	1 O1F3_CANFA	Q95156 canis faml
43	661	41.3	309	1 O1A2_HUMAN	Q95585 homo sapien
44	658	41.1	309	1 O1A1_PANTR	Q8ngt9 pan troglod
45	658	41.1	321	1 O5V1_HUMAN	Q9ugf6 homo sapien

ALIGNMENTS

RESULT 1

ID	O2AG_HUMAN	STANDARD	PRT	316 AA.
AC	Q9H205; Q96R26;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Olfactory receptor 2AG1 (HT3).			
GN	OR2AG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sauva M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,			
RA	Tsuetsumi S., Aburatani H., Asai K., Akiyama Y.;			
RT	"Genome-wide discovery and analysis of human seven transmembrane helix			
RT	receptor genes";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 68-284 FROM N.A.			
RX	MEDLINE=22202146; PubMed=12213199;			
RA	Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,			
RA	Shmulevich D., Elkon R., Steinfach M., O'Brien J.K., Radelof U.,			
RT	Lehnach H., Lancel D., Shamir R.;			
RT	"DEROG: a practical scheme for deciphering families of genes.";			
RL	Genomics 80:295-302(2002).			
RN	[3]			
RP	SEQUENCE OF 152-316 FROM N.A.			
RX	MEDLINE=21310002; PubMed=11416212;			
RA	Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,			
RA	Rowen L., Evans G., Axel R., Hood L., Trask B.J.;			
RT	"Genomic analysis of orthologous mouse and human olfactory receptor			
RT	loci.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).			
CC	- FUNCTION: Putative odorant receptor.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
CC	- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);			
CC	WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
DR	EMBL; AB065823; BAC06042.1; -			
DR	EMBL; AF399618; AAK95103.1; -			
DR	EMBL; AF321237; AAG45209.1; -			
DR	GeneW; HGNC:15142; OR2AG1.			
DR	InterPro; IPR00276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7cm_1; 1.			

RA Van den Nigh G., Demaille J.G., Giorgi D.;
 RT "Distribution of olfactory receptor genes in the human genome.";
 CC Nat. Genet. 18:243-250 (1998).
 RN [2].
 RP SEQUENCE OF 67-282 FROM N.A.
 RX MEDLINE=2202116; PubMed=12213199;
 RA Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
 RA Samulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
 RA Ishraek H., Lancel D., Shamir R.;
 RT "DEFOG: a practical scheme for deciphering families of genes.";
 CC Genomics 80:295-302 (2002).
 CC -I- FUNCTION: Putative odorant receptor.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -I- DATABASE: NAME=Human Olfactory Receptor Data Explorerium (HORED);
 CC WWW=http://bioinformatics.weismann.ac.il/cgi-bin/HORED/showgene.pl?key=symbol&
 CC
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 CC
 CC EMBL, U86215; AAC39611.1; --

Query Match	Best Local Similarity	Matches	Score	DB 1	Length	311
51.5%	52.1%	49	96	Indels	0	Gaps
158	Conervative	49	Mismatches	96	Indels	0
6	SLTGGSGILVGLINDSGSPRLVATFTIILMLTSGNLLLAITTEARILHMPYLLDGLQ	65				
5	NTSSDTDTFMGLPRKRTSGIIFALISIIFFTLMLANGWIIPLIQDRLRHTMYFLSH	64				
66	LSIMDLFTSVTPKALADFLRRNTISFGSCALQMFALITMGSABDLIAFMAVDRIVA	125				
65	LSLIDMVIISITVYKMLVNYLLDQRTISFVGCTAQPRLVYLLVGAEEFFLLGLMAYDRIVA	124				
126	ICHLKMTMLSPVVCIMVATSWIIASLAIIGHTWTYMLPCVSRIRPHLLCEIPILL	185				
125	ICNLRPVPVMSRRVCMIIAGSWFGSLDGLFLLTPIITMSFPCCNSKRNHPCEADAVL	184				
186	KLAACADSRRELLIYTVGVTFLLPLSAIVASYVLVFTVLRMPDSNEGRKKALVTGCSHL	245				
185	KLAACADRALIETWYVCCVIMLLIPSVLASIYARILITTYQCMSSVGRKKAFATGCSHM	244				


```

QY 246 IIVGMFYGAATFMYVLPSSFSPKONIIISFYITVPALNPLIYSLNKEVRRALRVY 305
DB 245 TVVSLFYGAATFMYVLPSSFSPKONIIISFYITVPALNPLIYSLNKEVRRALRVY 304
QY 306 GKY 308
DB 305 GRF 307

RESULT 3
0221 HUMAN STANDARD; PRT; 314 AA.
ID 0221 HUMAN
AC 08NG67; Q96R25; 42, Created
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 221.
GN OR221 OR OR222
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsubuni S., Aburatani H., Asai K., Akiyama Y.,
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RL receptor genes."
RL submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 68-284 FROM N.A.
RX MEDLINE=2202146; PubMed=1221319;
RA Fuchs T., Malcovova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radloff U.,
RA Lehnach H., Lancel D., Shamir R.;
RT "DEFOG: a practical scheme for deciphering families of genes.";
RL Genomics 80:295-302(2002).
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
-----
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-----
DR EMBL; AB065930; BAC06145.1; -
DR EMBL; AF399619; AAK95104.1; -
DR Genew; HGNC:15391; OR221.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1.1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25
FT TRANSMEM 26 49
FT DOMAIN 50 57
FT TRANSMEM 58 79
FT DOMAIN 80 100
FT TRANSMEM 101 120
FT DOMAIN 121 139
FT TRANSMEM 140 158
FT DOMAIN 159 195
FT TRANSMEM 196 219
FT DOMAIN 220 236

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FT TRANSMEM 237 259
FT DOMAIN 260 272
FT TRANSMEM 273 292
FT DOMAIN 293 314
FT CARBOHYD 5 5
SQ SEQUENCE 314 AA; 34444 MW; 537E389A5EDA471F CRC64;

Query Match
Best Local Similarity 50.8%; Score 816; DB 1; Length 314;
Matches 154; Conservative 55; Mismatches 94; Indels 0; Gaps 0;

QY 5 NSTLGGFTLVGILNDSSPELLIYATFTILYMLALTSNGLLATITERRILMPYLLG 64
DB 5 NQSVASDFLLVGLFHSRSGRQLLFSLVAFVYIGLIGTVLLFLRVDRILHMPYELL 64
QY 65 QSLMDLFTSVTPKALADFLRRENTSFGGCALOMPALMGSAEDLLFMAYDRY 124
DB 65 QSLMDLFTSVTPKALADFLRRENTSFGGCALOMPALMGSAEDLLFMAYDRY 124
QY 125 AICHPILKMTLMSPPVCMIVATSWILASLIAGHTMYTHLPFCVSWERHLLCEIPPL 184
DB 125 AICHPILKMTLMSPPVCMIVATSWILASLIAGHTMYTHLPFCVSWERHLLCEIPPL 184
QY 185 IRLACADTSRFFLLIYGVTFLLPLISAIYASYTLVFTVLRMPSEGRKALVTCSH 244
DB 185 IRLACADTSRFFLLIYGVTFLLPLISAIYASYTLVFTVLRMPSEGRKALVTCSH 244
QY 245 IIVGMFYGAATFMYVLPSSFSPKONIIISFYITVPALNPLIYSLNKEVRRALRVY 304
DB 245 IIVGMFYGAATFMYVLPSSFSPKONIIISFYITVPALNPLIYSLNKEVRRALRVY 304
QY 305 LCK 307
DB 305 LSR 307

RESULT 4
0272 HUMAN STANDARD; PRT; 323 AA.
ID 0272 HUMAN
AC 08NGX2;
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 272.
GN OR272.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsubuni S., Aburatani H., Asai K., Akiyama Y.,
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RL receptor genes."
RL submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
-----
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DR EMBL; AB065644; BAC05870.1; -
DR Genew; HGNC:14725; OR272.
DR InterPro; IPR000276; GPCR_Rhodopsn.

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RESULT 6
O2TB_HUMAN
ID O2TB_HUMAN STANDARD; PRT; 316 AA.
AC Q8NH01;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 2T11.
GN OR2T11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;

[1]
SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC MIM="http://biomimetics.weimann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC -----
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CC -----
DR EMBL; AB065614; BAC05841.1; -.
DR Genew; HGNC:19574; OR2T11.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECP_F1_1; FALISE_NEG.
DR PROSITE; PS0262; G PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 23 46 1 (POTENTIAL).
FT DOMAIN 47 54 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 55 76 2 (POTENTIAL).
FT DOMAIN 77 97 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 98 117 3 (POTENTIAL).
FT DOMAIN 118 136 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 137 155 4 (POTENTIAL).
FT DOMAIN 156 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 216 5 (POTENTIAL).
FT DOMAIN 217 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 256 6 (POTENTIAL).
FT DOMAIN 257 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 289 7 (POTENTIAL).
FT DOMAIN 290 316 CYTOPLASMIC (POTENTIAL).
FT DISULFID 94 186 BY SIMILARITY.
FT CARBOHYD 3 3 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 316 AA; 34797 MW; E785C0788F405FD8 CRC64;

Query Match 50.0%; Score 801; DB 1; Length 316;
Best Local Similarity 51.5%; Pred. No. 4,3e-51;
Matches 154; Conservative 54; Mismatches 91; Indels 0; Gaps 0;

OY 6 STLGSEFLLVGLNDGSEPELVATFTLLMALTSNGILLATITTEARLHPMYLLSQ 65
DB 3 NTSSSDFTLLGLVNSEAGIVFTVLAFLGAVTNLWIFLIQVDSRLHPMYLLSQ 62
OY 66 LSLMDLLFTSVTPKMLADEFLRENTISFGCAGLQWELAVTMGASDLLAFAYARYYA 125
DB 63 LSLMDLLFTSVTPKMLADEFLRENTISFGCAGLQWELAVTMGASDLLAFAYARYYA 122
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OY 126 ICHPLKMYTLMSPRCVIMWATSWILASLIALGHNTYTHLPFCVSEIRHLCEIPPLL 185
DB 123 VCNPLRYPYLMNRKCKLLAAGAFGSLDGFLLTPTLTMVVPYCGSRISINHFCIEPAVL 182
OY 186 KLAACDTSYELLIIYTGTFLLPLPSAIVASTVLVFLYLRPNSDEGRKKAIVTSSHL 245
DB 183 KLAACDTSYELLIIYTGTFLLPLPSAIVASTVLVFLYLRPNSDEGRKKAIVTSSHL 242
OY 246 IYVGFYGAATFMYVLPSSFSHPKODNIISVFITYTLPALNPLIYSLRNKEWRALRRV 304
DB 243 TVVSTFYGAATFYTVLPSSFSHPKODNIISVFITYTLPALNPLIYSLRNKEWRALRRV 301

RESULT 7
O2M6_HUMAN
ID O2M6_HUMAN STANDARD; PRT; 312 AA.
AC Q8NGS3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 2M6.
GN OR2M6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;

[1]
SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC MIM="http://biomimetics.weimann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC -----
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CC -----
DR EMBL; AB065952; BAC06165.1; -.
DR Genew; HGNC:19593; OR2M6.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 237 259 6 (POTENTIAL).
FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 273 292 7 (POTENTIAL).
FT DISULFID 293 311 CYTOPLASMIC (POTENTIAL).
FT 97 BY SIMILARITY.
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CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC -----
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CC -----
DR EMBL: AB065954; BAC06167.1; -
DR Genew; HGNC:19594; OR247.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 26 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 237 259 6 (POTENTIAL).
FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 273 292 7 (POTENTIAL).
FT DOMAIN 293 311 CYTOPLASMIC (POTENTIAL).
FT DISULFID 311 311 BY SIMILARITY.
FT CARBOHYD 97 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 312 AA; 34902 MW; 42A9A1D7EB861E88 CRC64;

Query Match 48.5%; Score 777; DB 1; Length 312;
Best Local Similarity 48.2%; Pred. No. 2.3e-49;
Matches 148; Conservative 51; Mismatches 108; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIVGLINDSGPELLVATFTLLMALTNSGILLATITTEARLHMPY 60
DB 1 MAMENQFNSDFLLGLIFNHSPTHTPLFVLALFVSVAFMGNSIMVLLIYDTQLHTPMY 60
QY 61 LLLGSLMDLFTSVTPKALDFLRRENTISFGGCAQMFALTMGSADLLAMAY 120
DB 61 FLISQSLMDLMLCTVPRKAFNYLSSKSIAMGACATQIFVYISLGSCEFLAAWSY 120
QY 121 DRYVAICHPKLYMTLSPRCVMIVATSWILASLAIIGHTMYTMHLPFCVSEIRHLCE 180
DB 121 DRYVAICHPKLYMTLSPRCVMIVATSWILASLAIIGHTMYTMHLPFCVSEIRHLCE 180
QY 181 IPPLLKACADTSRYELIYVTVFLPLISAVASYTLVFLVLPMSNEGKKA 240
DB 181 FPSLLISLNDSTISFEVIFICCIYMLVFPAIIITTSVAVILAVIHGSGEGRKAPT 240
QY 241 CSSHLIYVGMFYGAATPMYVLPSEFHSFKQNTISVFTTYTPALNPILYSLRKEV 300
DB 241 CSSHLIYVGMFYGAATPMYVLPSEFHSFKQNTISVFTTYTPALNPILYSLRKEV 300
QY 301 LRRVYLGK 307
DB 301 LRRVYLGK 307

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DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 274.
GN OR24.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tautumi S., Aburatani H., Asai K., Akiyama Y.;
RT "genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB065615; BAC05842.1; -
DR Genew; HGNC:15016; OR274.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 30 53 1 (POTENTIAL).
FT DOMAIN 54 61 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 62 83 2 (POTENTIAL).
FT DOMAIN 84 104 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 105 124 3 (POTENTIAL).
FT DOMAIN 125 143 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 144 162 4 (POTENTIAL).
FT DOMAIN 163 199 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 200 223 5 (POTENTIAL).
FT DOMAIN 224 240 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 241 263 6 (POTENTIAL).
FT DOMAIN 264 276 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 277 296 7 (POTENTIAL).
FT DOMAIN 297 320 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 193 BY SIMILARITY.
FT CARBOHYD 3 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 320 AA; 36124 MW; 501BCD4B237CF7D CRC64;

Query Match 48.4%; Score 776; DB 1; Length 320;
Best Local Similarity 50.2%; Pred. No. 2.8e-49;
Matches 152; Conservative 52; Mismatches 99; Indels 0; Gaps 0;

QY 3 LNSTLGSGLIVGLINDSGPELLVATFTLLMALTNSGILLATITTEARLHMPYLL 62
DB 7 MAMHTGMSDFLLGLFQSGKHPALLCVYIFVFMALSGNVALILLIHCHADHLTPMYEF 66
QY 63 LGLSLMDLFTSVTPKALDFLRRENTISFGGCAQMFALTMGSADLLAMAYDR 122
DB 67 ISQLSMDMAYISTVTPKMLLDQVGVKISAPBCGMQPFYVTLASGEFLATMAYDR 126
QY 123 YVATCHPKWMTLSPRCVMIVATSWILASLAIIGHTMYTMHLPFCVSEIRHLCEIP 182

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DR EMBL; AB065627; BAC05853.1; -
DR Genew; HGNC:15014; OR2L8.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24
FT TRANSMEM 25 48
FT DOMAIN 49 56
FT TRANSMEM 57 78
FT DOMAIN 79 99
FT TRANSMEM 100 119
FT DOMAIN 120 138
FT TRANSMEM 139 157
FT DOMAIN 158 194
FT TRANSMEM 195 218
FT DOMAIN 219 235
FT TRANSMEM 236 258
FT DOMAIN 259 271
FT TRANSMEM 272 291
FT DOMAIN 292 312
FT DISULFID 96 188
FT CARBOHYD 5 5
FT CARBOHYD 88 88
SQ SEQUENCE 312 AA; 35444 MW; 845325F98685AD4 CRC64;

Query Match
Best Local Similarity 46.7%; Score 747.5; DB 1; Length 312;
Matches 145; Conservative 49; Mismatches 109; Indels 1; Gaps 1;

QY 1 MELRNSTLGSGLFVGLINDSGSPPELLVATFTLLVMALTSNGLLLAATTEARLHPMY 60
DB 1 MERNVNT-STDFLLDLGPPPSRIDLPFLIYVFIMALIGMSMLLFLDTHATPMY 59
QY 61 LLLGQSLNDLFTSVVTEKALDFLRRENTISFGGCAQOMFLATMGSAEDLLAFMAY 120
DB 60 FLISQSLIDLVYISITVPRKMSDFLHGKKSISFTGCGISFFFLALGAEALLLASMAX 119
QY 121 DRVVAICHLKWTMLSPVRCWIMVATSWILASLAIHGTWTMLPCVSWEIRHLCE 180
DB 120 DRYIAICFLHYLIRMSKRCVLMITGWSIGSINACHTVYVLIHPCRSRAINHFCD 179
QY 181 IPELKLACADTSRYELIYVGVFLLPISAVASYLVLFYLRMSNGRKAAYT 240
DB 180 VPAAMTILACMDTWYIEGVFLSATITFLVPPFGISGYSQVLFAYHMSAAGRKAYLT 239
QY 241 CSSHLIVGMFYGAATFMYLPPSPKQDNIISVFTYIVPALNPLIYSIRNKVMA 300
DB 240 CSTHLTVVTFYAPFYVTLRPRSLRSPTEDKVANVFYIILPMNPIIYSIRNKVMA 299
QY 301 LRRV 304
DB 300 LTRV 303

RESULT 13
0212_HUMAN STANDARD; ERT; 312 AA.
AC Q8NHI6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 212 (HPRCH07).
GN OR2L2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Putani K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RA "Genome-wide discovery and analysis of human seven transmembrane helix
RA receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE OF 125-238 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=92131132; PubMed=1370853;
RA Parmentier M., Llobet F., Schumann S., Schiffmann S., Lefort A.,
RA Eggertick D., Ledent C., Mollereau C., Gerard C., Perret J.,
RA Grootegeed A., Vassart G.;
RT "Expression of members of the putative olfactory receptor gene family
RT in mammalian germ cells.";
RL Nature 355:453-455(1992).
CC - FUNCTION: Putative odorant receptor.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC - DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showgene.pl?key=symbol&
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DR EMBL; AB065597; BAC05825.1; -
DR EMBL; X64978; -; NOT ANNOTATED_CDS.
DR Genew; HGNC:8266; OR2L2.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24
FT TRANSMEM 25 48
FT DOMAIN 49 56
FT TRANSMEM 57 78
FT DOMAIN 79 99
FT TRANSMEM 100 119
FT DOMAIN 120 138
FT TRANSMEM 139 157
FT DOMAIN 158 194
FT TRANSMEM 195 218
FT DOMAIN 219 235
FT TRANSMEM 236 258
FT DOMAIN 259 271
FT TRANSMEM 272 291
FT DISULFID 96 188
FT CARBOHYD 5 5
FT CARBOHYD 88 88
SQ SEQUENCE 312 AA; 35495 MW; C85F0368D85CIDE CRC64;

Query Match
Best Local Similarity 45.8%; Score 733.5; DB 1; Length 312;
Matches 145; Conservative 52; Mismatches 109; Indels 1; Gaps 1;

QY 1 MELRNSTLGSGLFVGLINDSGSPPELLVATFTLLVMALTSNGLLLAATTEARLHPMY 60

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Db 1 MENYNOT-STDFILGIFPFSRIGLEVFTIFIFLALIGNSMILLIFDLHITPMV 59
QY 61 LLLGSLMDLFTSVTPPKALADFLRENTISFGGALOMFLATMGSAEDLLAFMAY 120
DB 60 FILSQSLIDANLSTIVPRGVDFLGKNSISFTGGIGSPFELLTAVAGELTSMAY 119
QY 121 DRYVALCHPKYMTLSPRCWIMWATSWLASLAIAGHTMYTMHLPFCWSMIRHLCE 180
DB 120 DRYVALCFPHYPIRISKRCVMMITGSMMISINSCAHTVALCLPYCKSRALNHFCD 179
QY 181 IPELKLACADTSRYELLIVYGVTFLLPISAIIVASYTLVFTVLMPSPNEGRKALVT 240
DB 180 VPAMLTACDITWYESTVFLSTIFLVLPFTGACGVGLAVYRMHSAEGRKKAYST 239
QY 241 CSSHLIVGMFYGAATFMYLPSFSFKODNIISVFTYTPALNPLIYSLRKEVMRA 300
DB 240 CSTHLIVVSFYAPFAYTVRPRSLRSPEDKILAVFTYTLTPLNPIIYSLRKEVMA 299
QY 301 LRRVLGK 307
DB 300 LRVVIGK 306

RESULT 14
O2A1_HUMAN STANDARD; PRT; 310 AA.
AC Q8NGT9; Q96R46;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 2A1.
GN OR2A1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 67-283 FROM N.A.
RX MEDLINE=2202146; PubMed=12211199;
RA Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA LeFrach H., Lancel D., Shamir R.;
RT "DEFOG: a practical scheme for deciphering families of genes.";
RL Genomics 80:295-302(2002).
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NMBE=human Olfactory Receptor Data Explorer (HORDX);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDX/showGene.pl?key=symbols
CC
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CC
CC EMBL; AB065692; BAC05915.1; ALT_INIT.
CC EMBL; AF199597; AAK95082.1;
CC Genew; HGNC:8229; OR2A1.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHDODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.

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DR PROSITE; PS00262; G PROTEIN RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 78 2 (POTENTIAL).
FT DOMAIN 79 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 119 3 (POTENTIAL).
FT TRANSMEM 120 138 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 139 157 4 (POTENTIAL).
FT TRANSMEM 158 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 218 5 (POTENTIAL).
FT TRANSMEM 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 258 6 (POTENTIAL).
FT TRANSMEM 259 271 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 272 291 7 (POTENTIAL).
FT TRANSMEM 292 310 CYTOPLASMIC (POTENTIAL).
FT DISULFID 96 188 BY SIMILARITY.
FT CARBOHYD 4 4 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 310 AA; 34714 MW; CSE0170B025B871 CRC64;

Query Match 45.0%; Score 721; DB 1; Length 310;
Best Local Similarity 46.2%; Pred. No. 2.5e-45;
Matches 140; Conservative 53; Mismatches 110; Indels 0; Gaps 0;

QY 5 NSTTSGFVLVGLINDSGPELVATFTIYMLATNSGLLALITTEARLHMPVLLG 64
DB 4 NOTWTFEFLIGFLGLGRIGRMFLGSLFYITLIGNGAILGLISDLSLHPMVEFLS 63
QY 65 QLSIMDLFTSVTPPKALADFLRENTISFGGALOMFLATMGSAEDLLAFMAYDRYV 124
DB 64 HLAVIDIAYTRNTVPQMLANLHPAKRISPAGCMTQFCLISGSHSECLLVMSYDRYV 123
QY 125 AICHPLKMTLMBRVYMWATSWLASLAIAGHTMYTMHLPFCWSMIRHLCEIPL 184
DB 124 AICHPLKYSVIMRWVCITLAVTSWTCGSLALAHVLLIRLPSPGHEINHFCEILSV 183
QY 185 IKLACADTSRYELLIVYGVTFLLPISAIIVASYTLVFTVLMPSPNEGRKALVTCSSH 244
DB 184 LRLACATWLNQVITPAFCYFLVGPSSLVVYSHTLAIIRIQSGEGRKRASTCSSH 243
QY 245 LIVGMFYGAATFMYLPSFSFKODNIISVFTYTPALNPLIYSLRKEVMRAIRRV 304
DB 244 LCVGLFPGSALIVYMAFKSRHPKQKVFPLFYSPFNPTLNPILYSLRKEVGAALRA 303
QY 305 LGK 307
DB 304 LGK 306

RESULT 15
O2B_HUMAN STANDARD; PRT; 312 AA.
AC Q8NG80;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 2B1.
GN OR2B1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

```



```
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -1- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC -----
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CC -----
DR EMBL; AB065956; BAC06169.1; -
DR GenBank; HGNC:19570; OR2L11.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1.1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 78 2 (POTENTIAL).
FT DOMAIN 79 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 119 3 (POTENTIAL).
FT DOMAIN 120 138 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 139 157 4 (POTENTIAL).
FT DOMAIN 158 194 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 195 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 258 6 (POTENTIAL).
FT DOMAIN 259 271 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 272 291 7 (POTENTIAL).
FT DOMAIN 292 312 CYTOPLASMIC (POTENTIAL).
FT DISULFID 96 188 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GICNAC...) (POTENTIAL).
SQ SEQUENCE 312 AA; 35648 MW; E04FEB75A902863 CRC64;

Query Match 44.5%; Score 713.5; DB 1; Length 312;
Best Local Similarity 46.2%; Pred. No. 8.8e-45;
Matches 141; Conservative 50; Mismatches 113; Indels 1; Gaps 1;

QY 1 MEIRNSTLGSGFTLVGILNDGSPPELLATFTILYMLATISNGLLLATITTEARLHPMY 60
DB 1 MENYQT-STDFILGLPSPKIGLFLFLIFLIFLMALIGNLMLIFLDTLHTPMY 59
QY 61 ILLGQLSMDLLEFVSVPKALADFLRENTISFGCALQWFLALTMGSAEDLLAFMY 120
DB 60 FLISQLSLIDLNYISTIVPKASDPLVGNKKSISFICGQISFFMTFAGAEALLITSMAY 119
QY 121 DRYVAICHPLKMYTMSPRVCWIVATSWILASLAIIGHWTYTMHLPFCVSEIRHLCE 180
DB 120 DRYVAICFPLHPYRMSKRMVYLMITGSMIGSINSCAHYARIPYCKSRAINHFCD 179
QY 181 IPPLLAKACADTSRELLIYTGVTPLLPISAIYASTVLVFTVLRMPDSNEGRKALVT 240
DB 180 VPAMTLTACTVTWYEVFLSTIFLVFPFGIACSYGWLAVYRMHSAEGRKAYST 239
QY 241 CSSHLIVGMFGATFMVLPSSSPKODIISVFYIVTPANPLIYSIRNKEVRA 300
DB 240 CSTHTLVTFYAPAYTLCPRSLRSLTEKVALVFTYITLPMINPITIYSLRNKEVGA 299
QY 301 LRRVYL 305
DB 300 LTRVYL 304
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Search completed: August 18, 2004, 08:57:07
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 08:36:58 ; Search time 78 Seconds

(without alignments)
1278.253 Million cell updates/sec

Title: US-10-024-444B-2

Sequence: 1 MELNSTLGGSLVGLIND.....VMRLRVLGVKYLIASTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriap:*
17: SP archaep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1324	82.6	316	11 Q9EPF8	Q9EPF8 mus musculu
2	1312	81.9	316	11 Q9D3U9	Q9D3U9 mus musculu
3	1308	81.6	316	11 Q8VGT0	Q8VGT0 mus musculu
4	1308	81.6	316	11 Q9D4F9	Q9D4F9 mus musculu
5	1305	81.5	316	11 Q9D4F9	Q9D4F9 mus musculu
6	1304	81.4	316	11 Q9EPF7	Q9EPF7 mus musculu
7	1276	79.7	316	11 Q8VPM5	Q8VPM5 mus musculu
8	1248	77.9	316	11 Q9EPF5	Q9EPF5 mus musculu
9	1243	77.6	315	11 Q8VPM8	Q8VPM8 mus musculu
10	1236	77.2	311	11 Q7TRN4	Q7TRN4 mus musculu
11	1230	76.8	311	11 Q8VPM6	Q8VPM6 mus musculu
12	1210.5	75.6	315	11 Q8VPM3	Q8VPM3 mus musculu
13	1205	75.2	316	11 Q8VPM3	Q8VPM3 mus musculu
14	1204	75.2	317	11 Q8VPM4	Q8VPM4 mus musculu
15	1203	75.1	315	11 Q9EPF6	Q9EPF6 mus musculu
16	1178	73.5	316	11 Q7TRN3	Q7TRN3 mus musculu

17	846	52.8	317	11 Q8VGD7	Q8VGD7 mus musculu
18	839	52.4	314	11 Q7TRX2	Q7TRX2 mus musculu
19	836	52.2	315	11 Q8VGD8	Q8VGD8 mus musculu
20	836	52.2	317	11 Q8VGT5	Q8VGT5 mus musculu
21	833	52.0	317	4 Q8NH04	Q8NH04 homo sapien
22	824	51.4	314	11 Q7TRX1	Q7TRX1 mus musculu
23	822	51.3	308	11 Q8VPM8	Q8VPM8 mus musculu
24	816	50.9	320	11 Q7TRZ2	Q7TRZ2 mus musculu
25	811	50.6	323	4 Q8NGX2	Q8NGX2 mus musculu
26	809.5	50.5	335	11 Q7TRX7	Q7TRX7 mus musculu
27	808	50.4	312	11 Q7TRX0	Q7TRX0 mus musculu
28	806	50.3	314	11 Q7TRX8	Q7TRX8 mus musculu
29	801	50.0	316	4 Q8NH01	Q8NH01 homo sapien
30	800	49.9	310	11 Q7TRZ1	Q7TRZ1 mus musculu
31	798	49.8	310	11 Q8VPM6	Q8VPM6 mus musculu
32	795	49.6	309	11 Q7TRX9	Q7TRX9 mus musculu
33	795	49.6	315	11 Q8VGD9	Q8VGD9 mus musculu
34	794	49.6	312	4 Q8NG83	Q8NG83 mus musculu
35	793	49.5	320	4 Q8NG84	Q8NG84 mus musculu
36	785	49.0	313	11 Q7TS53	Q7TS53 mus musculu
37	780	48.7	313	11 Q7TS51	Q7TS51 mus musculu
38	779	48.6	314	11 Q8VGL7	Q8VGL7 mus musculu
39	777	48.5	312	4 Q8NG81	Q8NG81 homo sapien
40	771.5	48.2	312	11 Q7TS52	Q7TS52 mus musculu
41	771.5	48.2	313	11 Q8VGL6	Q8VGL6 mus musculu
42	771	48.1	306	11 Q7TRZ6	Q7TRZ6 mus musculu
43	771	48.1	306	11 Q7TRZ4	Q7TRZ4 mus musculu
44	770	48.1	312	4 Q8NG29	Q8NG29 homo sapien
45	767	47.9	316	11 Q8VPM3	Q8VPM3 mus musculu

ALIGNMENTS

RESULT 1

Q9EPF8 PRELIMINARY; PRT; 316 AA.

AC Q9EPF8; 01-MAR-2001 (TREMURel. 16, Created)
DT 01-MAR-2001 (TREMURel. 16, Last sequence update)
DT 01-OCT-2003 (TREMURel. 25, Last annotation update)
DE T1 olfactory receptor (Olfactory receptor MOR283-11) (Olfactory receptor GA_X6K02T2PB39-9271198-9270248).
GN GA_X6K02T2PB39-9271198-9270248.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C., Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
RN (2)
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 0:0-0(2002).
RN (3)
RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RA Young J.M., Shykink B.M., Lane R.P., Tonnes-Priddy L., Ross J.A., Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400 genes, extensive alternate splicing, and unequal expression levels."
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.

RN [5]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AR321234; ANG45195.1; -
 DR EMBL; AY073740; AAL61403.1; -
 DR EMBL; AY17827; AAP71171.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 316 AA; 34981 MW; 5D89HPIBEH17D480 CRC64;
 Query Match 82.6%; Score 1324; DB 11; Length 316;
 Best Local Similarity 82.3%; Pred. No. 6e-110;
 Matches 260; Conservative 23; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MELNSTLGGSGFIVGILINDSGSPPELLYATFTIYMLALTSNGLLIATITTEARLMPY 60
 DB 1 MELNSTLGGSGFIVGILINDSGSPPELLYATFTIYMLALTSNGLLIATITTEARLMPY 60
 QY 61 LILGQSLMDLFTSVVTPKALADFLRENTISFGCALQMFALTMGSAEDLLAFMAY 120
 DB 61 LILGQSLMDLFTSVVTPKALADFLRENTISFGCALQMFALTMGSAEDLLAFMAY 120
 QY 61 LILRQSLIDLFTSVVTPKAMDFILRDNTISFGCALQMFALTMGSAEDLLAFMAY 120
 DB 61 LILRQSLIDLFTSVVTPKAMDFILRDNTISFGCALQMFALTMGSAEDLLAFMAY 120
 QY 121 DRYVALCHPLKMTLMSPRVCMWVATSWILASILAIGHYTMHLPCVSWEIRHLICE 180
 DB 121 DRYVALCHPLKMTLMSPRVCMWVATSWILASILAIGHYTMHLPCVSWEIRHLICE 180
 QY 121 DRYVALCHPLKMTLMSPRVCMWVATSWILASILAIGHYTMHLPCVSWEIRHLICE 180
 DB 121 DRYVALCHPLKMTLMSPRVCMWVATSWILASILAIGHYTMHLPCVSWEIRHLICE 180
 QY 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIYASYTLVLFYLRMPSNEGRKKALVT 240
 DB 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIYASYTLVLFYLRMPSNEGRKKALVT 240
 QY 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIYASYTLVLFYLRMPSNEGRKKALVT 240
 DB 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIYASYTLVLFYLRMPSNEGRKKALVT 240
 QY 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRKEVRA 300
 DB 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRKEVRA 300
 QY 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRKEVRA 300
 DB 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRKEVRA 300
 QY 301 LRRVLGKTYLLAHSTL 316
 DB 301 LRRVLGKTYLLAHSTL 316
 QY 301 LRRVLGKTYLLAHSTL 316
 DB 301 LRRVLGKTYLLAHSTL 316
 RESULT 2
 Q9D3U9 PRELIMINARY; PRT; 316 AA.
 ID Q9D3U9
 AC 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE 4933433602rik protein (Olfactory receptor MOR283-1) (Olfactory receptor GA_x6K02T2PB9-9195805-9196755)
 GN 4933433602RIK OR GA_X6K02T2PB9-9195805-9196755.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai U., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hata A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa Y., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml U.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gardoloi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [2]
 RP SEQUENCE FROM N.A.
 RA Zhang S.J.; Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 [3]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykina B.M., Lane R.P., Tomes-Pridy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK017036; BAB30564.1; -
 DR EMBL; AY073025; AAL60688.1; -
 DR EMBL; AY17822; AAP71166.1; -
 DR MGI; MGI:1914036; 4933433602rik.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 316 AA; 34916 MW; C2C538B675D3225 CRC64;
 Query Match 81.9%; Score 1312; DB 11; Length 316;
 Best Local Similarity 80.4%; Pred. No. 7e-109;
 Matches 254; Conservative 29; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MELNSTLGGSGFIVGILINDSGSPPELLYATFTIYMLALTSNGLLIATITTEARLMPY 60
 DB 1 MELNSTLGGSGFIVGILINDSGSPPELLYATFTIYMLALTSNGLLIATITTEARLMPY 60
 QY 1 MELNSTLGGSGFIVGILINDSGSPPELLYATFTIYMLALTSNGLLIATITTEARLMPY 60
 DB 1 MELNSTLGGSGFIVGILINDSGSPPELLYATFTIYMLALTSNGLLIATITTEARLMPY 60
 QY 61 LILGQSLMDLFTSVVTPKALADFLRENTISFGCALQMFALTMGSAEDLLAFMAY 120
 DB 61 LILGQSLMDLFTSVVTPKALADFLRENTISFGCALQMFALTMGSAEDLLAFMAY 120
 QY 61 LILRQSLIDLFTSVVTPKAMDFILRDNTISFGCALQMFALTMGSAEDLLAFMAY 120
 DB 61 LILRQSLIDLFTSVVTPKAMDFILRDNTISFGCALQMFALTMGSAEDLLAFMAY 120
 QY 121 DRYVALCHPLKMTLMSPRVCMWVATSWILASILAIGHYTMHLPCVSWEIRHLICE 180
 DB 121 DRYVALCHPLKMTLMSPRVCMWVATSWILASILAIGHYTMHLPCVSWEIRHLICE 180
 QY 121 DRYVALCHPLKMTLMSPRVCMWVATSWILASILAIGHYTMHLPCVSWEIRHLICE 180
 DB 121 DRYVALCHPLKMTLMSPRVCMWVATSWILASILAIGHYTMHLPCVSWEIRHLICE 180
 QY 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIYASYTLVLFYLRMPSNEGRKKALVT 240
 DB 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIYASYTLVLFYLRMPSNEGRKKALVT 240
 QY 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIYASYTLVLFYLRMPSNEGRKKALVT 240
 DB 181 IPLPLKACADTSRYELIYVTVGTFLLPLISAIYASYTLVLFYLRMPSNEGRKKALVT 240
 QY 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRKEVRA 300
 DB 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRKEVRA 300
 QY 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRKEVRA 300
 DB 241 CSSHLIVGMFYGAATFMYVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRKEVRA 300
 QY 301 LRRVLGKTYLLAHSTL 316
 DB 301 LRRVLGKTYLLAHSTL 316
 QY 301 LRRVLGKTYLLAHSTL 316
 DB 301 LRRVLGKTYLLAHSTL 316

DB 301 VRRVIGRHILPAHATV 316

RESULT 3

OSVU00 PRELIMINARY; PRT; 316 AA.

AC OSVU00;

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Olfactory receptor MOR283-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;

RT "The olfactory receptor gene superfamily of the mouse.";

RL Nat. Neurosci. 0:0-0(2002).

RN [2]

RP SEQUENCE FROM N.A.

RA Adams M.;

RU Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY073056; AAL60719.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_2; 1.

DR KMW Receptor.

SQ SEQUENCE 316 AA; 35239 MW; 2E05EB6642A34C6 CRC64;

Query Match 81.6%; Score 1308; DB 11; Length 316;

Best Local Similarity 80.4%; Pred. No. 1.6e-108;

Matches 254; Conservative 29; Mismatches 33; Indels 0; Gaps 0;

QY 1 MELRNSTLGSGLVIGLINDSGSPPELLVATFTLLVMTALTSNGLLALATTEARLHPMY 60

DB 1 MEPMNSTLGSGLVIGLINDSGSPPELLCATFTLLVMTALTSNGLLALATTEARLHPMY 60

QY 61 LLLGQLSLMDLFTSVTPKALADFLRRNTISFGGCAIQMFALTMGSAEDLLAFMY 120

DB 61 LLLGQLSLMDLFTSVTPKALADFLRRNTISFGGCAIQMFALTMGSAEDLLAFMY 120

QY 121 DRYVALCHPLKMTLMSPRVCIWATSWILASLAIAGHTMYTMLPFCVSEIRHLCE 180

DB 121 DRYVALCHPLKMTLMSPRVCIWATSWILASLAIAGHTMYTMLPFCVSEIRHLCE 180

QY 181 IPPLLKACADTSREYLIIYVGVTELLPISAIYASYTLVLFYLRMSNGRKKALVT 240

DB 181 IPPLLKACADTSREYLIIYVGVTELLPISAIYASYTLVLFYLRMSNGRKKALVT 240

QY 241 CSSHLIVGMFYGATFMVLPSSSPKQDNIIISVFYITVPALNPLIYSLRNKEVMA 300

DB 241 CSSHLIVGMFYGATFMVLPSSSPKQDNIIISVFYITVPALNPLIYSLRNKEVMA 300

QY 301 LRRVLGKYLILAHSTL 316

DB 301 LRRVLGKYLILAHSTL 316

DB 301 LRRVLGKYLILAHSTL 316

RESULT 4

Q9D4F9 PRELIMINARY; PRT; 316 AA.

AC Q9D4F9;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE 4932441H2IRik protein.

GN 4933433E02RIK OR 4932441H2IRIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Testis;

RC MEDLINE=21085660; PubMed=11217851;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Iawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batzloff S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schirml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Guelincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilting L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK016560; BAB30304.1; -

DR MCD; MG1:1914036; 4933433E02RIK.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_2; 1.

SQ SEQUENCE 316 AA; 34930 MW; 231E8FBA8C207BA CRC64;

Query Match 81.6%; Score 1308; DB 11; Length 316;

Best Local Similarity 80.1%; Pred. No. 1.6e-108;

Matches 253; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 1 MELRNSTLGSGLVIGLINDSGSPPELLVATFTLLVMTALTSNGLLALATTEARLHPMY 60

DB 1 MEPMNSTLGSGLVIGLINDSGSPPELLCATFTLLVMTALTSNGLLALATTEARLHPMY 60

QY 61 LLLGQLSLMDLFTSVTPKALADFLRRNTISFGGCAIQMFALTMGSAEDLLAFMY 120

DB 61 LLLGQLSLMDLFTSVTPKALADFLRRNTISFGGCAIQMFALTMGSAEDLLAFMY 120

QY 121 DRYVALCHPLKMTLMSPRVCIWATSWILASLAIAGHTMYTMLPFCVSEIRHLCE 180

DB 121 DRYVALCHPLKMTLMSPRVCIWATSWILASLAIAGHTMYTMLPFCVSEIRHLCE 180

QY 181 IPPLLKACADTSREYLIIYVGVTELLPISAIYASYTLVLFYLRMSNGRKKALVT 240

DB 181 IPPLLKACADTSREYLIIYVGVTELLPISAIYASYTLVLFYLRMSNGRKKALVT 240

QY 241 CSSHLIVGMFYGATFMVLPSSSPKQDNIIISVFYITVPALNPLIYSLRNKEVMA 300

DB 241 CSSHLIVGMFYGATFMVLPSSSPKQDNIIISVFYITVPALNPLIYSLRNKEVMA 300

QY 301 LRRVLGKYLILAHSTL 316

DB 301 LRRVLGKYLILAHSTL 316

DB 301 LRRVLGKYLILAHSTL 316

RESULT 5

Q7TRN2 PRELIMINARY; PRT; 316 AA.

AC Q7TRN2;

Q7TRN2

01-OCT-2003 (TREMblrel. 25, Created)
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Olfactory receptor GA_x6K02T2PBj9-9255348-9255398.
 GN GA_x6K02T2PBj9-9255348-9255398.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tomes-Priddy L., Rose J.A.,
 Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor Esrs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels."
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL EMBL; AY317826; AAF71170.1; -.
 KW RECEPTOR.
 SQ SEQUENCE 316 AA; 35266 MW; 6318EB66443EB21D CRC64;
 Query Match 81.5%; Score 1305; DB 11; Length 316;
 Best Local Similarity 80.1%; Pred. No. 3e-108;
 Matches 253; Conservative 30; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MELNSTLGSGLTNGILNDSGSPPELLYATFTTLYMALTSNGLLIATITEARLHMPY 60
 DB 1 MEPMNSTLGTDFNLVGLDSDGSPPELLCATFTALYMLALISNGLLIATITMDARLHMPY 60
 QY 61 LLIGQLSIMDLFTSVTPKALADFLRENTISFGGALQMPALTMGSAEDLLATMAY 120
 DB 61 FLIGQLSIMDLFTSVTPKAVIDFLRDNTISFGGSLQMPALTMGSAEDLLATMAY 120
 QY 121 DRYAICHPLKMTLSPRCVMTWATSWLASLAIAGHTMYTMHLPCVSWETRIHLCE 180
 DB 121 DRYAICHPLNMYTLMSPRCVMTWATSWLASLAIAGHTMYTMHLPCVSWETRIHLCE 180
 QY 181 IPLLKLAACDTSRELIIVTGVTFLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 DB 181 IPLLKLAACDTSRELIIVTGVTFLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 QY 241 CSSHLIVGMFYGATFMVLPSSFHSFKODNIIISVFYITVPALNPLIYSLRKEVRA 300
 DB 241 CSSHLIVGMFYGATFMVLPSSFHSFKODNIIISVFYITVPALNPLIYSLRKEVRA 300
 QY 301 LRRVIGKTYILAHSTL 316
 DB 301 LRRVIGKTYILAHSTL 316
 QY 301 LIRVIGRYIVPAHPTL 316
 DB 301 LIRVIGRYIVPAHPTL 316
 RESULT 6
 Q9EPF7 PRELIMINARY; PRT; 316 AA.
 ID Q9EPF7;
 AC Q9EPF7;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
 DE T2 olfactory receptor.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J;
 RA MEDLINE=21310002; PubMed=11416212;
 RA Lane R.P., Outforth T., Young J., Athanasios M., Friedman C.,
 RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
 RT "Genomic analysis of orthologous mouse and human olfactory receptor
 loci."

Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
 DR EMBL; AF21234; AAG45196.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_P1_2; 1.
 KW RECEPTOR.
 SQ SEQUENCE 316 AA; 35252 MW; B5029F55D161A1E CRC64;
 Query Match 81.4%; Score 1304; DB 11; Length 316;
 Best Local Similarity 79.7%; Pred. No. 3.6e-108;
 Matches 252; Conservative 31; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MELNSTLGSGLTNGILNDSGSPPELLYATFTTLYMALTSNGLLIATITEARLHMPY 60
 DB 1 MEPMNSTLGTDFNLVGLDSDGSPPELLCATFTALYMLALISNGLLIATITMDARLHMPY 60
 QY 61 LLIGQLSIMDLFTSVTPKALADFLRENTISFGGALQMPALTMGSAEDLLATMAY 120
 DB 61 FLIGQLSIMDLFTSVTPKAVIDFLRDNTISFGGSLQMPALTMGSAEDLLATMAY 120
 QY 121 DRYAICHPLKMTLSPRCVMTWATSWLASLAIAGHTMYTMHLPCVSWETRIHLCE 180
 DB 121 DRYAICHPLNMYTLMSPRCVMTWATSWLASLAIAGHTMYTMHLPCVSWETRIHLCE 180
 QY 181 IPLLKLAACDTSRELIIVTGVTFLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 DB 181 IPLLKLAACDTSRELIIVTGVTFLLPISAIIVASYTLVFTVLRMPNSNEGRKALVT 240
 QY 241 CSSHLIVGMFYGATFMVLPSSFHSFKODNIIISVFYITVPALNPLIYSLRKEVRA 300
 DB 241 CSSHLIVGMFYGATFMVLPSSFHSFKODNIIISVFYITVPALNPLIYSLRKEVRA 300
 QY 301 LRRVIGKTYILAHSTL 316
 DB 301 LRRVIGKTYILAHSTL 316
 QY 301 LIRVIGRYIVPAHPTL 316
 DB 301 LIRVIGRYIVPAHPTL 316
 RESULT 7
 Q9VFM5 PRELIMINARY; PRT; 316 AA.
 ID Q9VFM5;
 AC Q9VFM5;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Olfactory receptor MOR283-4 (Olfactory receptor
 GN GA_x6K02T2PBj9-9184187-9184237).
 GN GA_x6K02T2PBj9-9184187-9184237.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RT Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tomes-Priddy L., Rose J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor Esrs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels."
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073497; AAL61160.1; -;
 DR EMBL; AY317821; AAP71165.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR KMW Receptor.
 SQ SEQUENCE 316 AA; 35283 MW; 3D944A8FA1A7436 CRC64;
 Query Match 79.7%; Score 1276; DB 11; Length 316;
 Best Local Similarity 78.1%; Pred. No. 1,1e-105;
 Matches 246; Conservative 31; Mismatches 38; Indels 0; Gaps 0;
 QY 1 MELNSTLGSGLVGLINDSGPELLYATFTLLYMLATNSGLLALTTEARLHMPY 60
 DB 1 MELNSTLGSGLVGLINDSGPELLYATFTLLYMLATNSGLLALTTEARLHMPY 60
 QY 61 LLLGQSLMDLFTSVTPKALADFLRENTISFGCALOMFLATMGSAEDLLAFMAY 120
 DB 61 LLLGQSLMDLFTSVTPKALADFLRENTISFGCALOMFLATMGSAEDLLAFMAY 120
 QY 121 DRVVALCHPLKNTLMSPRVCIMVATSWILASILAIGHMTYTMHLPCVSWEIRHLCE 180
 DB 121 DRVVALCHPLKNTLMSPRVCIMVATSWILASILAIGHMTYTMHLPCVSWEIRHLCE 180
 QY 181 IPELKLKACADTSREYELIIVTGVTFLLPISAIVASYTLVFTVLRMSENGRKKALVT 240
 DB 181 IPELKLKACADTSREYELIIVTGVTFLLPISAIVASYTLVFTVLRMSENGRKKALVT 240
 QY 241 CSNHLIVGMFYGAATFMVLPSSFSHPKODNISVFYITVPALNPLIYSLRNKEVMA 300
 DB 241 CSNHLIVGMFYGAATFMVLPSSFSHPKODNISVFYITVPALNPLIYSLRNKEVMA 300
 QY 301 LRRVIGKYLILAHST 315
 DB 301 LRRVIGKYLILAHST 315
 RESULT 8
 Q9EPF5 PRELIMINARY; PRT; 319 AA.
 ID Q9EPF5;
 AC Q9EPF5;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE T4 olfactory receptor (Olfactory receptor MOR283-7) (Olfactory receptor GA_X6K02T2PBj9-9222217-9223176).
 GN GA_X6K02T2PBj9-9222217-9223176.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21310002; PubMed=11416212;
 RA Lane R.P., Outforth T., Young J., Athanasiou M., Friedman C., Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
 RT "Genomic analysis of orthologous mouse and human olfactory receptor loci."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).

RP [3]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A., Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor B6TS demonstrate olfactory expression of over 400 genes, extensive alternate splicing, and unequal expression levels."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF212234; AAG45198.1; -;
 DR EMBL; AY073501; AAL61164.1; -;
 DR EMBL; AY317824; AAP71168.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR KMW Receptor.
 SQ SEQUENCE 319 AA; 35493 MW; 8CFB7EC7A5BDD3D8 CRC64;
 Query Match 77.3%; Score 1248; DB 11; Length 319;
 Best Local Similarity 75.4%; Pred. No. 3.6e-103;
 Matches 236; Conservative 37; Mismatches 40; Indels 0; Gaps 0;
 QY 1 MELNSTLGSGLVGLINDSGPELLYATFTLLYMLATNSGLLALTTEARLHMPY 60
 DB 1 MELNSTLGSGLVGLINDSGPELLYATFTLLYMLATNSGLLALTTEARLHMPY 60
 QY 61 LLLGQSLMDLFTSVTPKALADFLRENTISFGCALOMFLATMGSAEDLLAFMAY 120
 DB 61 LLLGQSLMDLFTSVTPKALADFLRENTISFGCALOMFLATMGSAEDLLAFMAY 120
 QY 121 DRVVALCHPLKNTLMSPRVCIMVATSWILASILAIGHMTYTMHLPCVSWEIRHLCE 180
 DB 121 DRVVALCHPLKNTLMSPRVCIMVATSWILASILAIGHMTYTMHLPCVSWEIRHLCE 180
 QY 181 IPELKLKACADTSREYELIIVTGVTFLLPISAIVASYTLVFTVLRMSENGRKKALVT 240
 DB 181 IPELKLKACADTSREYELIIVTGVTFLLPISAIVASYTLVFTVLRMSENGRKKALVT 240
 QY 241 CSNHLIVGMFYGAATFMVLPSSFSHPKODNISVFYITVPALNPLIYSLRNKEVMA 300
 DB 241 CSNHLIVGMFYGAATFMVLPSSFSHPKODNISVFYITVPALNPLIYSLRNKEVMA 300
 QY 301 LRRVIGKYLILAH 313
 DB 301 LRRVIGKYLILAH 313
 RESULT 9
 Q8VF88 PRELIMINARY; PRT; 315 AA.
 ID Q8VF88;
 AC Q8VF88;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE Olfactory receptor MOR283-9 (Olfactory receptor GA_X6K02T2PBj9-9067220-9068273).
 GN GA_X6K02T2PBj9-9067220-9068273.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]

RA SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "the olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Townes-Priddy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Yask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073646; AAL61309.1; -
 DR EMBL; AY317815; AAP71160.1; -
 DR GO; GO:0016021; C:Integral to membrane, IEA.
 DR GO; GO:0004872; F:receptor activity, IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity, IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF000001; 7cm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 315 AA; 34927 MW; 9A9E426357BA710C CRC64;

Query Match 77.6%; Score 1243; DR 11; Length 315;
 Best Local Similarity 78.8%; Pred. No. 9,9e-103;
 Matches 242; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

QY 1 MELRSTLGGSGFLLVGLINDSGSPFLVATFTLLYMLALTSNGLLLAITTEARLAMPY 60
 DB 1 MEVCNSTLSSGILLVGLINDSGFPELLCATITALLFLAITSGLLLVITMDARLHVPMY 60
 QY 61 LILIGQLSLMDLFTSVTPKALADFLRRENTISFGGCAIQMFLALTMGSAEDLLAFMAY 120
 DB 61 LILMQSLMDLILTSVTPKALIDYLLKQNTISFGGCAIQMFLLEVLGSAEDLLAFMAY 120
 QY 121 DRYVALCHPLKTYMTLMSPRVCMVATSWILASLIALGHTMTMHLPCVSWEIRHLCE 180
 DB 121 DRYVALCHPLANTYMTLMSQKVCIMATSWILASLMSLGSIYTMQYPFCKSQIRHLCE 180
 QY 181 IPELLTLACADSRVRELLIYTVGPELLPISAIVASLYTLVFTYLRMPSNGRKALVY 240
 DB 181 IPELLTLACADSRVRELLIYTVGPELLPISAIVASLYTLVFTYLRMPSNGRKALVY 240
 QY 241 CSSEHLIVGMFGYGAATFMYVLPSSEFSPKQDNISVFTYITVPALNPLIYSIRNKEVMA 300
 DB 241 CSSEHLIVGMFGYGAATFMYVLPSSEFSPKQDNISVFTYITVPALNPLIYSIRNKEVMA 300
 QY 301 LRRVLGK 307
 DB 301 LRRVLGK 307

RESULT 10
 Q7TRN4 PRELIMINARY; PRT; 311 AA.
 ID 07TRN4
 AC 07TRN4
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Olfactory receptor GA_x6K02T2PB9J-9130754-9129519.
 GN GA_x6K02T2PB9J-9130754-9129519.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Axel R., Trask B.J.;
RT "odorant receptor ESTs demonstrate olfactory expression of over 400
RT genes, extensive alternate splicing, and unequal expression levels."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY317819; AAF1163.1; -.
KW Receptor.
SQ SEQUENCE 311 AA; 34182 MW; 1338254FA2F8D21D CRC64;

Query Match 77.2%; Score 1236; DB 11; Length 311;
Best Local Similarity 77.9%; Pred. No. 4.1e-102;
Matches 239; Conservative 31; Mismatches 37; Indels 0; Gaps 0

QY 1 MELNSTGSGFIVGILNDSGSPFLIYAFITLIYMLALTNSGLLLATITTEARLHPMY 60
D 1 MELNNTYGGSGFIIYGLIDGSSPELLCAIYALYFIALTSNGLLVITMDARLHPMY 60
QY 61 LILGQLSLMDILFTSVTPPKALADFLRRENTISFGGCAIQMFALTMGSAEDLLAFMY 120
D 61 LILGQLSLMDILFTSVTPPKAAVDFLLKDNITISFGGCAIQMFALTMGSAEDLLAFMY 120
QY 121 DRYVACHPKLKMTLMSPRVCIMVATSWILSLIAGHTMYTHLPFCVSWEIRHLCE 180
D 121 DRYVACHPPLNVTILMSHVCMVLTATSWILSLSLAGSYITMYQYSPCKNRINHLFCE 180
QY 181 IPELKLKACADPSREYELIYVGVFELLIPISAVSYTLVETVLMPSENGRKLAVT 240
D 181 IPELKLKACADPSREYELIYVGVFELLIPISAVSYTLVETVLMPSENGRKLAVT 240
QY 241 CSSHLIVGMFYGAATPMYVLPFSRHSPEKODNISVFYITVTPALNPLIYSLNKEVMA 300
D 241 CSSHLIVGMFYGAATPMYVLPFSRHSPEKODNISVFYITVTPALNPLIYSLNKEVMA 300
DY 301 LRRVIGK 307
DY 301 LRRVIGK 307

RESULT 11
Q8VFME PRELIMINARY; PRT; 311 AA.
ID Q8VFME
AC Q8VFME;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, last annotation update)
DE Olfactory receptor MOR283-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY073495; AAL61158.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR Interpro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS50262; G_PROTEIN_RECIP_FL_2; 1.
 KW RECEPTOR

Query Match 311 AA; 34194 MW; 901137C8BF8D20C CRC64;
 Best Local Similarity 76.8%; Score 1230; DB 11; Length 311;
 Matches 238; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

QY 1 MELNSTGSGFIIIVGILNDGSPPELLYATFTIYMLATNSGILLATITTEARLHMPY 60
 DB 1 MELNSTGSGFIIIVGILNDGSPPELLCAITLALYFLATNSGILLATITTEARLHMPY 60
 QY 61 LILGQSLMDLFLSVTPPKALDFLRRENTISGGCALQWFLALMGSAEDLLAFMAY 120
 DB 61 LILGQSLMDLFLSVTPPKALDFLRRENTISGGCALQWFLALMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPKMYTLMSPRCVIMVATSWILASIALGHTMYTMHLPCVSWETRIHCE 180
 DB 121 DRYVAICHPKMYTLMSPRCVIMVATSWILASIALGHTMYTMHLPCVSWETRIHCE 180
 QY 181 IPELKLACADTSRYELIIVTGVTFLLPISAVASYTLVFTVLMPSNEGRKKALVT 240
 DB 181 IPELKLACADTSRYELIIVTGVTFLLPISAVASYTLVFTVLMPSNEGRKKALVT 240
 QY 241 CSSHLIVGMFYGAATMYVLPSSFHSPKODNITSVFTYITVPALNPLIYSLNKEYWRA 300
 DB 241 CSSHLIVGMFYGAATMYVLPSSFHSPKODNITSVFTYITVPALNPLIYSLNKEYWRA 300
 QY 301 LRRVLGK 307
 DB 301 LRRVLGK 307

RESULT 12

Q8VFM3
 ID 08VFM3 PRELIMINARY; PRT; 315 AA.

AC 08VFM3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Olfactory receptor MOR283-6 (Olfactory receptor
 GA_X6K02T2PBJ9-9092181-9091234).
 GN GA_X6K02T2PBJ9-9092181-9091234.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Priddy L., Rose J.A.,
 RA Walker M., Williams B.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA EMBL; AY073499; AAL61162.1; -;
 DR EMBL; AY073499; AAL61162.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS50262; G_PROTEIN_RECIP_FL_2; 1.
 KW RECEPTOR

Query Match 315 AA; 35179 MW; AC02001D73D1736 CRC64;
 Best Local Similarity 75.6%; Score 1210.5; DB 11; Length 315;
 Matches 237; Conservative 31; Mismatches 46; Indels 1; Gaps 1;

QY 1 MELNSTGSGFIIIVGILNDGSPPELLYATFTIYMLATNSGILLATITTEARLHMPY 60
 DB 1 MELNSTGSGFIIIVGILNDGSPPELLCAITLALYFLATNSGILLATITTEARLHMPY 60
 QY 61 LILGQSLMDLFLSVTPPKALDFLRRENTISGGCALQWFLALMGSAEDLLAFMAY 120
 DB 61 LILGQSLMDLFLSVTPPKALDFLRRENTISGGCALQWFLALMGSAEDLLAFMAY 120
 QY 121 DRYVAICHPKMYTLMSPRCVIMVATSWILASIALGHTMYTMHLPCVSWETRIHCE 180
 DB 121 DRYVAICHPKMYTLMSPRCVIMVATSWILASIALGHTMYTMHLPCVSWETRIHCE 180
 QY 181 IPELKLACADTSRYELIIVTGVTFLLPISAVASYTLVFTVLMPSNEGRKKALVT 240
 DB 181 IPELKLACADTSRYELIIVTGVTFLLPISAVASYTLVFTVLMPSNEGRKKALVT 240
 QY 241 CSSHLIVGMFYGAATMYVLPSSFHSPKODNITSVFTYITVPALNPLIYSLNKEYWRA 300
 DB 241 CSSHLIVGMFYGAATMYVLPSSFHSPKODNITSVFTYITVPALNPLIYSLNKEYWRA 300
 QY 301 LRRVLGK 315
 DB 301 LRRVLGK 315

RESULT 13

Q8VFM3
 ID 08VFM3 PRELIMINARY; PRT; 316 AA.

AC 08VFM3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Olfactory receptor MOR283-8 (Olfactory receptor
 GA_X6K02T2PBJ9-9055944-9054994).
 GN GA_X6K02T2PBJ9-9055944-9054994.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tomnes-Priddy L., Rose J.A.,
 RA Walker M., Williams B.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA EMBL; AY073645; AAL61308.1; -;
 DR EMBL; AY073645; AAL61308.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0004872; P: receptor activity; IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS: PR00237; GPCR_Rhodpsn.
 DR PROSITE: PS50262; G_PROTEIN_RECER_F1_2; 1.
 KM RECEPTOR
 KM SEQUENCE 316 AA; 35153 MW; 2123AF7831AFA228 CRC64;
 Query Match 75.2%; Score 1205; DB 11; Length 316;
 Best Local Similarity 73.8%; Pred. No. 2.4e-99;
 Matches 231; Conservative 36; Mismatches 46; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLVIGLINDSGSPFLVATFTIYMLALTSNGILLATITAEALHMPY 60
 DB 1 MEPNSTLGSGLVIGLINDSGSPFLVATFTIYMLALTSNGILLATITAEALHMPY 60
 QY 61 LLLGSLIMDLFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLIAFMAY 120
 DB 61 LLLGSLIMDLFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLIAFMAY 120
 QY 121 DRYVAICHLKMYTMSPRVCIMVATSWILASLAIQHTMYMLPCVSWETRHLC 180
 DB 121 DRYVAICHLKMYTMSPRVCIMVATSWILASLAIQHTMYMLPCVSWETRHLC 180
 QY 181 IPELLKACADTSRELYITVGTFTLLPISAIYASTVLFTVLRMPSNEGRKALVT 240
 DB 181 IPELLKACADTSRELYITVGTFTLLPISAIYASTVLFTVLRMPSNEGRKALVT 240
 QY 241 CSSHLIVGMFYGATFMYVLPSSFSHPKODNIIISVFYITVPALNPPIYSIRNKEVRA 300
 DB 241 CSSHLIVGMFYGATFMYVLPSSFSHPKODNIIISVFYITVPALNPPIYSIRNKEVGA 300
 QY 301 LRRVLGKYLLLAH 313
 DB 301 LRRVLGKYLLLAH 313
 QY 301 LRRVLGKYLLLAH 313
 DB 301 LRRVLGKYLLLAH 313

RESULT 14
 Q8VFEM4 PRELIMINARY; PRT; 317 AA.
 AC Q8VFEM4
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Olfactory receptor MOR283-5 (Olfactory receptor
 DE GA X6K02T2PB3J-9119301-9118348).
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN NCB1
 RN SEQUENCE FROM N.A.
 RN "Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN NCB1
 RN SEQUENCE FROM N.A.
 RN [1]
 RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RN Young J.M., Shykind B.M., Lane R.P., Tonnes-Priiddy L., Ross J.A.,
 RA Walker M., Williams B.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RN Sanders K.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY073498; AAL61161.1; -
 DR EMBL: AY317818; AAP71162.1; -
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0004872; P: receptor activity; IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS: PR00237; GPCR_Rhodpsn.
 DR PROSITE: PS50262; G_PROTEIN_RECER_F1_2; 1.
 KM RECEPTOR
 KM SEQUENCE 317 AA; 35471 MW; C5F1B706E5437F73 CRC64;
 Query Match 75.2%; Score 1204; DB 11; Length 317;
 Best Local Similarity 75.5%; Pred. No. 3e-99;
 Matches 231; Conservative 29; Mismatches 46; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLVIGLINDSGSPFLVATFTIYMLALTSNGILLATITAEALHMPY 60
 DB 1 MEPNSTLGSGLVIGLINDSGSPFLVATFTIYMLALTSNGILLATITAEALHMPY 60
 QY 61 LLLGSLIMDLFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLIAFMAY 120
 DB 61 LLLGSLIMDLFTSVTPKALADFLRENTISFGCALQMFALITMGSAEDLLIAFMAY 120
 QY 121 DRYVAICHLKMYTMSPRVCIMVATSWILASLAIQHTMYMLPCVSWETRHLC 180
 DB 121 DRYVAICHLKMYTMSPRVCIMVATSWILASLAIQHTMYMLPCVSWETRHLC 180
 QY 181 IPELLKACADTSRELYITVGTFTLLPISAIYASTVLFTVLRMPSNEGRKALVT 240
 DB 181 IPELLKACADTSRELYITVGTFTLLPISAIYASTVLFTVLRMPSNEGRKALVT 240
 QY 241 CSSHLIVGMFYGATFMYVLPSSFSHPKODNIIISVFYITVPALNPPIYSIRNKEVRA 300
 DB 241 CSSHLIVGMFYGATFMYVLPSSFSHPKODNIIISVFYITVPALNPPIYSIRNKEVGA 300
 QY 301 LRRVLG 306
 DB 301 LRRVLG 306
 QY 301 LRRVLG 306
 DB 301 LRRVLG 306

RESULT 15
 Q9EPF6 PRELIMINARY; PRT; 315 AA.
 AC Q9EPF6
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE T3 olfactory receptor (Olfactory receptor
 DE GA X6K02T2PB3J-9247095-9248042).
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN NCB1
 RN SEQUENCE FROM N.A.
 RN STRAIN=C57BL/6J;
 RX MEDLINE=21310002; PubMed=11416212;
 RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,
 RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
 RT "Genomic analysis of orthologous mouse and human olfactory receptor
 RT loci.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RN Young J.M., Shykind B.M., Lane R.P., Tonnes-Priiddy L., Ross J.A.,
 RA Walker M., Williams B.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels.";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

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OM protein - protein search, using sw model

Run on: August 18, 2004, 08:55:13 ; Search time 19 Seconds

(without alignments)
858,621 Million cell updates/sec

Title: US-10-024-444B-2

Sequence: 1602
1 MELRNSTLGSGLVGLIND.....VNRALRVKLTILAHSTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	49.4	316	2	US-08-827-291A-2
2	668	41.7	321	3	US-08-748-506-12
3	666	41.6	321	3	US-08-748-506-20
4	663.5	41.4	321	3	US-08-748-506-10
5	661.5	41.3	321	3	US-08-748-506-13
6	661.5	41.3	321	3	US-08-748-506-18
7	644	40.2	340	4	US-09-546-986A-6
8	644	40.2	340	4	US-09-524-730-6
9	643	40.1	321	3	US-08-748-506-19
10	642	40.1	223	4	US-09-465-901-40
11	642	40.1	321	3	US-08-748-506-11
12	632	39.5	314	3	US-08-988-876-7
13	616	38.5	334	4	US-09-546-986A-8
14	616	38.5	334	4	US-09-524-730-8
15	605	37.8	310	4	US-09-546-986A-2
16	605	37.8	310	4	US-09-524-730-2
17	595.5	37.2	313	4	US-09-465-901-48
18	582	36.3	284	1	US-08-118-270-61
19	582	36.3	284	5	PCT-US93-08528-61
20	577.5	36.0	296	2	US-08-467-948A-2
21	577.5	36.0	296	3	US-08-467-948A-2
22	576	36.0	333	3	US-08-988-876-6
23	575	35.9	309	3	US-08-988-876-5
24	575	35.9	331	4	US-09-546-986A-4
25	575	35.9	331	4	US-09-524-730-4
26	565.5	35.3	284	1	US-08-118-270-67
27	565.5	35.3	284	5	PCT-US93-08528-67

28	563	35.1	223	4	US-09-465-901-24	Sequence 24, Appl
29	558	34.8	223	4	US-09-465-901-20	Sequence 20, Appl
30	558	34.8	223	4	US-09-465-901-28	Sequence 28, Appl
31	534.5	33.4	274	1	US-08-118-270-69	Sequence 69, Appl
32	534.5	33.4	274	5	PCT-US93-08528-69	Sequence 69, Appl
33	516	32.2	277	1	US-08-118-270-68	Sequence 68, Appl
34	516	32.2	277	5	PCT-US93-08528-68	Sequence 68, Appl
35	512.5	32.0	286	1	US-08-118-270-65	Sequence 65, Appl
36	512.5	32.0	286	5	PCT-US93-08528-65	Sequence 65, Appl
37	507	31.6	247	1	US-08-465-980-3	Sequence 3, Appl1
38	507	31.6	247	2	US-09-053-303-3	Sequence 3, Appl1
39	507	31.6	247	4	US-09-339-115-3	Sequence 3, Appl1
40	507	31.6	247	5	PCT-US93-07093-3	Sequence 3, Appl1
41	500	31.2	223	4	US-09-465-901-38	Sequence 38, Appl
42	496.5	31.0	222	2	US-08-467-948A-27	Sequence 27, Appl
43	496.5	31.0	222	3	US-08-467-948A-27	Sequence 27, Appl
44	495.5	30.9	293	1	US-08-118-270-60	Sequence 60, Appl
45	495.5	30.9	293	5	PCT-US93-08528-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-08-827-291A-2
; Sequence 2, Application US/08827291A
; Patent No. 5874243
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; TITLE OF INVENTION: NOVEL OLRC15 RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: US
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,291A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GP50001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-827-291A-2
Query Match 49.4%; Score 792; DB 2; Length 316;
Best Local Similarity 49.5%; Pred. No. 7,8e-65;
Matches 152; Conservative 49; Mismatches 106; Indels 0; Gaps 0;
CY 1 MELRNSTLGSGLVGLINDSGPELLYATFTILYMLATNSGILLATITTEARLHMEY 60

Db 1 MARENTHSDFIKGIENHSPHTLFLVLAIFSAFMGNSVWLLIYDQHTPMX 60
 QY 61 LILGQISLMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSAEDLLAFMA 120
 Db 61 LILGQISLMDLFTSVTPKALADFLRRENTISFGGALOMFLATMGSAEDLLAFMA 120
 QY 121 DRVVAICHPKXWTLMSPRCWMVATSWMLASLIAGHTMYMHLPCVSWERHLLCE 180
 Db 121 DRVVAICHPKXWTLMSPRCWMVATSWMLASLIAGHTMYMHLPCVSWERHLLCE 180
 QY 181 IPELKLKACADTSRYELIIVTGVTFLLPISAIVASVTLVLTFLRMPSEGRKALVT 240
 Db 181 IPELKLKACADTSRYELIIVTGVTFLLPISAIVASVTLVLTFLRMPSEGRKALVT 240
 QY 241 CSSHLIVGMFGAATFMYLPSFSHPKODNISVFTYVTPALNPLYSLRNKXVMA 300
 Db 241 CSSHLIVGMFGAATFMYLPSFSHPKODNISVFTYVTPALNPLYSLRNKXVMA 300
 QY 301 LRRVLGK 307
 Db 301 LRRVLGK 307
 QY 301 FMKISGK 307
 Db 301 FMKISGK 307

RESULT 2

US-08-748-506-12
 / Sequence 12, Application US/08748506
 / Patent No. 6139707
 / GENERAL INFORMATION:
 / APPLICANT: Romnett et al.
 / TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 / NUMBER OF SEQUENCES: 31
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Leydig, Volt & Mayer, Ltd.
 / STREET: Two Prudential Plaza, Suite 4900
 / CITY: Chicago
 / STATE: IL
 / COUNTRY: US
 / ZIP: 60601-6780
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/748,506
 / FILING DATE: 08-NOV-1996
 / CLASSIFICATION: 435
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 60/033,751
 / FILING DATE: 09-NOV-1995
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / REFERENCE/DOCKET NUMBER: 74940
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 312-616-5600
 / TELEFAX: 312-616-5700
 / INFORMATION FOR SEQ ID NO: 12:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 321 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-748-506-12

Query Match 41.7%; Score 668; DB 3; Length 321;
 Best Local Similarity 47.3%; Pred. No. 1.8e-53;
 Matches 133; Conservative 42; Mismatches 106; Indels 0; Gaps 0;

QY 26 LLYATFTILYMLATNSGLLATTIERARLHMPYLLIGQISLMDLFTSVTPKALAD 85
 Db 32 LLYATFTILYMLATNSGLLATTIERARLHMPYLLIGQISLMDLFTSVTPKALAD 85

QY 86 LRRENTISFGGALOMFLATMGSAEDLLAFMAVDRYVAICHPKXWTLMSPRCWMV 145
 Db 92 VSEARGISWEGCASQMFPIFGITECCLAAAFDRYVAICSPHLVATRRMSRGVCAVLA 151
 QY 146 ATSWILASLIAGHTMYMHLPCVSWERHLLCEIPPLKLKACADTSRYELIIVTGV 205
 Db 152 IYSWVGICVGLGQNFIFSLNFCPCEDIDHFCDDLPPLALCGDTSQNEAIFPAVVL 211
 QY 206 FLPLPISAIVASVTLVLTFLRMPSEGRKALVTCSSHLIVGMFGAATFMYLPSFS 265
 Db 212 CIFSPFLLISSSVRLVAVLWMPSEGRKALVTCSSHLIVTFLFGTSATYLRSSKS 271
 QY 266 HSPKODNISVFTYVTPALNPLYSLRNKXVMA 306
 Db 272 HSPGVDKLALFYTSTVSMPLIYSLRNKXVMA 312

RESULT 3

US-08-748-506-20
 / Sequence 20, Application US/08748506
 / Patent No. 6139707
 / GENERAL INFORMATION:
 / APPLICANT: Romnett et al.
 / TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 / NUMBER OF SEQUENCES: 31
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Leydig, Volt & Mayer, Ltd.
 / STREET: Two Prudential Plaza, Suite 4900
 / CITY: Chicago
 / STATE: IL
 / COUNTRY: US
 / ZIP: 60601-6780
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/748,506
 / FILING DATE: 08-NOV-1996
 / CLASSIFICATION: 435
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 60/033,751
 / FILING DATE: 09-NOV-1995
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / REFERENCE/DOCKET NUMBER: 74940
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 312-616-5600
 / TELEFAX: 312-616-5700
 / INFORMATION FOR SEQ ID NO: 20:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 321 amino acids
 / TYPE: amino acid
 / TOPOLOGY: unknown
 / MOLECULE TYPE: protein
 / US-08-748-506-20

Query Match 41.6%; Score 666; DB 3; Length 321;
 Best Local Similarity 47.3%; Pred. No. 2.7e-53;
 Matches 133; Conservative 42; Mismatches 106; Indels 0; Gaps 0;

QY 26 LLYATFTILYMLATNSGLLATTIERARLHMPYLLIGQISLMDLFTSVTPKALAD 85
 Db 32 LLYATFTILYMLATNSGLLATTIERARLHMPYLLIGQISLMDLFTSVTPKALAD 85
 QY 86 LRRENTISFGGALOMFLATMGSAEDLLAFMAVDRYVAICHPKXWTLMSPRCWMV 145
 Db 92 VSEARGISWEGCASQMFPIFGITECCLAAAFDRYVAICSPHLVATRRMSRGVCAVLA 151
 QY 146 ATSWILASLIAGHTMYMHLPCVSWERHLLCEIPPLKLKACADTSRYELIIVTGV 205
 Db 152 IYSWVGICVGLGQNFIFSLNFCPCEDIDHFCDDLPPLALCGDTSQNEAIFPAVVL 211


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Sequence 18: Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSER: Leydig, Voigt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-748-506-18

Query Match 41.3%; Score 661.5; DB 3; length 321;
Best Local Similarity 47.9%; Pred. No. 7e-53;
Matches 137; Conservative 39; Mismatches 109; Indels 1; Gaps 1

QY 26 LLYATFTTIVVLMALTSNGLLIATITIEARLHMPYLLIGOLSLMDLFTSVTPRALAD 85
Db 32 LLEFNLILMFVLSLGNLLIYALITSTPSLHPTMVFLLANLSLHIGTCSVIPRLQSL 91
QY 86 LRENTISFGGCAOLMFTALTMGSAEDLLAFMAYDRVVAICHPLKWTMSPRKWTM 145
Db 92 VSEAREISREGCATOMFEFFAFGITECCILAMAFDRCMATCSPLHATVMSREVCALHA 151
QY 146 ATSWILASLILAHMTMYMHLPEFCWSIEIRHLGCEIPPLTKACADTSRYELIIVTGV 205
Db 152 IVSWMGCVISIGQTNFIFSLNFCGPCIIDHFCDDPLPILALACGDTSONEALITVAVL 211
QY 206 FLLEPISAIIVASYTLVLFPTVLRMPSENGRKKALVTCSSHLIVGMFYGAATMYVLPSSF 265
Db 212 CISSPFLILIVSYVILLIIVILMPPEGRHKALSTCSSHLIVVTLFYGSACITVLRPKSS 271
QY 266 HSPKODNIIISVYTYTVPALNPLIISLNKEVMRLRPVLG-KYLL 310
Db 272 HSPGMDKFLALFYIVVTSMLNPLIIVSLRNKEVKAALRRTLGKLL 317

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        TITLE OF INVENTION: No. 6635741el G-Protein Coupled Receptors
        FILE REFERENCE: 018781-004720US
        CURRENT APPLICATION NUMBER: US/09/546, 986A
        PRIOR FILING DATE: 2002-04-30
        PRIOR APPLICATION NUMBER: US 09/524, 730
        PRIOR FILING DATE: 2000-03-14
        NUMBER OF SEQ ID NOS: 16
        SOFTWARE: PatentIn Ver. 2.1
        SEQ ID NO: 6
        LENGTH: 340
        TYPE: PRT
        ORGANISM: Homo sapiens
    US -09-546-986A-6

Query Match      40.2%; Score 644; DB 4; Length 340;
Best Local Similarity 41.2%; Pred. No. 3e-51;
Matches 127; Conservative 65; Mismatches 110; Indels 6; Gaps 2;

QY          1 MELNRSTGSGFIIVGLINDSGSPPELLVATFTIL---VMALTSNGILLATTIEARLHM 57
            |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db           22 MEIANVSSPEVFVLGF--SARSLETVELFIVLSRFWMSILDGGIIIVSHDVDHLHT 78

QY          58 PMYLIGQLSLMDLLFTSVTPPKALADFLRRNTISFGCALQMFLATMGSAEDDLIAF 117
            |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db           79 PMVEFFLANIIFLDMSGFTTSSIPQLAMIMGPDKITSYGGCVGDFEYSIHMLGATECVLLAT 138

QY          118 MAIDRYVAIGHPLKXYMTLMSPRCWMINAVASMIASLIAIGHMYVTMELPRCSMEIRHL 177
            |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db           139 MSYRKYAIKRPHLYTVTIMHPOLCLGLALSWSLGTLTWGSQTILMLPFCGNDCIDHF 198

QY          178 LCEIPPLKLKA CADTSREYELLIVTGTFLLDPTISAASYTLVLFVL RMP SNEGRKA 237
            |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db           199 FCHEPFLMQACVDLTSLNEMENVIASFVVLPGLGLIVSGHIALRAVALXIKRSABGRKA 258

QY          238 LVTCSSHLIIVGMFYGAATEPVYVPSSFHSFKODNIISVETTYTPALNPILIYSRKNEY 297
            |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db           259 FNCTSSHVAAVSRLFYGSIIFYWLQPAKSTS HOKKFIALFTYV VTPALNP ILYLR NTEV 318

QY          298 MRAIRRVL 305
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Db           319 KSALARHW 326

RESULT 8
US-09-524-730-6
Sequence 6, Application US/09524730
Patent No. 6638733
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPlicant: Yang, Jianxin
ApplicAnt: Cutler, Gene
ApplICAnT: Tuttle Inc.
FILE REFERENCE: 018781-004710US
CURRENT APPLICATION NUMBER: US/09/524, 730
CURReNT FIling DAtE: 2000-03-14
NUMBER Of Seq Id Nos: 16
SOftwAre: PatentIn Ver. 2.1
SEQ ID NO: 6
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-09-524-730-6

Query Match      40.2%; Score 644; DB 4; Length 340;
Best Local Similarity 41.2%; Pred. No. 3e-51;
Matches 127; Conservative 65; Mismatches 110; Indels 6; Gaps 2

QY          1 MELNRSTGSGFIIVGLINDSGSPPELLVATFTIL---VMALTSNGILLATTIEARLHM 57
            |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db           22 MEIANVSSPEVFVLGF--SARPSELETVLVISFWVISILGNGIITLVSHTTDVHLHT 78

QY          58 PMYLIGQLSLMDLLFTSVTPPKALADFLRRNTISFGCALQMFLATMGSAEDDLIAF 117
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Db 79 PMVFPLANISFLMSFTTISVLPOLLANMGPQKTISVGGCVQFYISHMLGAIECVILAT 138
Qy 118 MAYDRVAICHPKXTMTLSPRCVCMVATSWILASLIAGHTMYTMHLPCVSWETRHL 177
Db 139 MSYDRVAICHPKXTMTLSPRCVCMVATSWILASLIAGHTMYTMHLPCVSWETRHL 198
Qy 178 LGEIPLMLKACADTSRYELIIVVTGVTLLPISAIIVASYTIVLFTVLRMPSENGRKA 237
Db 199 FCEMPLIMQACVDTISLNMEMVLASFVFPVPLGLIVSYGHIAVAKIRSAEGRRA 258
Qy 238 LVTCSHLLIVGMFYGAATFMYVLPSSFSHPKODNIISVYTTVPALNPLIYSLRKEV 297
Db 259 FMTCSGHVAVSLFYSGIIFMTIQPKASHGKRIALFYVTVTALNPLIYTLNTEV 318
Qy 298 MPALRRVL 305
Db 319 KSALRRMV 326

RESULT 9

US-08-748-506-19
Sequence 19, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-748-506-19

Query Match 40.1%; Score 643; DB 3; Length 321;
Best Local Similarity 46.4%; Pred. No. 3,5e-51;
Matches 130; Conservative 39; Mismatches 111; Indels 0; Gaps 0;
Qy 26 LLYATFTLMLATLNSGLILATITELAHMPVTLILGOLSTIMDLFTSVTPKALADF 85
Db 32 LLLFTLLMLFLVSLTGNALIALACTSPSLHPTMFLANISLTLIGTCTVTPMLQSL 91
Qy 86 LRENTTIFGGCALOMFLATLNGSABDILLAFMAYDRVAICHPKXTMTLSPRCVMTW 145
Db 92 VSEANEISREGCATOMFFFTFGITECCILAMAFDRCGICSPHIVATRMSEVCAHLA 151

Qy 146 ATSMILASLIAGHTMYTMHLPCVSWETRHLCEIPLPLKACADTSRYELIIVTGT 205
Db 152 IYSWGCGICVIGQGTNNIISLNFCCGCEIDHFECDPLPLALACGPTSQNEAIFVAAL 211
Qy 206 FLLPLISAIIVASYTIVLFTVLRMPSENGRKKALVTCSSHLIYVGMFYGAATFMYVLPSSF 265
Db 212 CISPFLVILSYRILVAVLWPSPEGRKALSTSSHLVLTLYFGSVSFTYLRKSS 271
Qy 266 HSPKODNIISVYTTVPALNPLIYSLRKEVYALRRVL 305
Db 272 HSPGMDKLALFYTAVTSMLNPLIYSLRKEVYALRRVL 311

RESULT 10

US-09-465-901-40
Sequence 40, Application US/09465901
Patent No. 6492143
GENERAL INFORMATION:
APPLICANT: Reed, Randall
APPLICANT: Yau, King-Wai
APPLICANT: Krautwurst, Dietmar
TITLE OF INVENTION: Olfactory Receptor Expression Libraries
FILE REFERENCE: 001107,00105
CURRENT APPLICATION NUMBER: US/09/465,901
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/112,605
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 223
TYPE: PR
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: PCR primer
US-09-465-901-40

Query Match 40.1%; Score 642; DB 4; Length 223;
Best Local Similarity 55.7%; Pred. No. 2,8e-51;
Matches 123; Conservative 29; Mismatches 69; Indels 0; Gaps 0;
Qy 66 ISMLPLFTSVTPKALADFRENTISFGGALOMFLATLNGSABDILLAFMAYDRVA 125
Db 3 LSFIDMAYISTIVPMLVDYILGQRTISFVGCTAGHFLYTLVGAEPFLGLMAYDRVA 62
Qy 126 ICHPKXTMTLSPRCVCMVATSWILASLIAGHTMYTMHLPCVSWETRHLCEIPL 185
Db 63 ICHPKXTMTLSPRCVCMVATSWILASLIAGHTMYTMHLPCVSWETRHLCEIPL 122
Qy 186 KACADTSRYELIIVVTGVTLLPISAIIVASYTIVLFTVLRMPSENGRKKALVTCSSHL 245
Db 123 KACADTSRYELIIVVTGVTLLPISAIIVASYTIVLFTVLRMPSENGRKKALVTCSSHL 182
Qy 246 IYVGMFYGAATFMYVLPSSFSHPKODNIISVYTTVPALN 286
Db 183 TVTLYFGAATYVWPVSHSPSODKIFSVYTTVLTPLN 223

RESULT 11

US-08-748-506-11
Sequence 11, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US

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      ZIP: 60601-6780
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/748,506
      FILING DATE: 08-NOV-1996
      CLASSIFICATION: 435
      PRIORITY APPLICATION DATA:
      APPLICATION NUMBER: US 60/033,751
      FILING DATE: 09-NOV-1995
      CLASSIFICATION: 435
      ATTORNEY/AGENT INFORMATION: 74940
      REFERENCE/DOCKET NUMBER:
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 312-616-5600
      TELEFAX: 312-616-5700
      INFORMATION FOR SEQ ID NO: 11:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 321 amino acids
      TYPE: amino acid
      STRANDEDNESS: unknown
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      US-08-748-506-11

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Query Match      40.1%; Score 642, DB 3, Length 321,
Best Local Similarity 46.4%; Pred. No. 4.3e-51;
Matches 130; Conservative 38; Mismatches 112; Indels 0; Gaps 0;

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QY 26 LLYATFLLMLALTSNGLLLAITTEARLHMPYLLLGSLIMDLFTSVVPMKALAD 85
DB 32 LFTLLMLLVSILTGALLALAXCTSPSLHTPYFPLANLSLEIGYTSVLPKQLSL 91
QY 86 LRRENTISFGGCAIOMFLATMGSABDLILAFMAYDRYVAICHLKMYLMSPRVCIMV 145
DB 92 VSRAREISRGCAIQMFFFTFRTBCCLLAAMAFDRCMGICSLPHATMSREVCNLA 151
QY 146 ATSMILASLIAGHTMYTMHLPCVSWIEIRHLLCEIPPLIKACADTSRYELIYVTGT 205
DB 152 IVSMGMCIVGLQGTNIXISLNFQPCIEIDHFCDLPPLALACGDTSQNEAIFVAAIL 211
QY 206 FLLPLISAIYASTIVLFTYLRMPSNKGKALVTCSSHLIVGMFGAFPMVLPSSF 265
DB 212 CISSPFLVILYSYRILIVAVLWMPSPGRKHALSTCSSHLVLTFLYGSVFTYLRKSS 271
QY 266 HSPKODNIIISVFTYTPALNPLIYSLRNKVMKALRRVL 305
DB 272 HSPGMDKLIALFYTAIVSMINFIYSLRNKVMKALRRVL 311

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RESULT 12
US-08-988-876-7
Sequence 7, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:

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      MEDIUM TYPE: Diskette
      COMPUTER: IBM Compatible
      OPERATING SYSTEM: DOS
      SOFTWARE: PASTSEQ for Windows Version 2.0
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/988,876
      FILING DATE: Herewith
      CLASSIFICATION:
      PRIORITY APPLICATION DATA:
      APPLICATION NUMBER:
      FILING DATE:
      ATTORNEY/AGENT INFORMATION:
      NAME: Billings, Lucy J.
      REGISTRATION NUMBER: 36,749
      REFERENCE/DOCKET NUMBER: PF-0441 US
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 650-855-0555
      TELEFAX: 650-845-4166
      INDEX:
      INFORMATION FOR SEQ ID NO: 7:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 314 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      IMMEDIATE SOURCE:
      LIBRARY: GenBank
      CLONE: 32086
      US-08-988-876-7

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Query Match      39.5%; Score 632, DB 3, Length 314,
Best Local Similarity 41.4%; Pred. No. 3.4e-50;
Matches 125; Conservative 57; Mismatches 120; Indels 0; Gaps 0;

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QY 4 RNTLSGFLVIGINDSGSPELLVNTFTLMLALTSNGLLALTTEARLHMPYLL 63
DB 4 QNTSISDFLLLPLOPEQONLCYALFLAMYITLLGNLLIYVLRHDSHLRPMYLL 63
QY 64 GOLSLMDLFTSVVTPKALADFLRRENTISFGGCAIOMFLATMGSABDLILAFMAYDRY 123
DB 64 SNISFDLCRSSSTIRPLQNMQNDPSIYACDCTQMYFLLFGDESLFLVAMAYDRY 123
QY 124 VAIICHLKYMTLMSPRVCIMVATSWILASLIAGHTMYTMHLPCVSWIEIRHLLCEIP 183
DB 124 VAICFPLHYAIMSPMLCLALVALSWLTFHMLHTLIMARLCFCADNVIPIHFCDMSA 183
QY 184 LKTLACADTSRYELIYVTGVTLLPISAIYASTIVLFTYLRMPSNKGKALVTCSS 243
DB 184 LKTLAEDTVNMEVAVIFIMGGLIIVLPFLILGSYARIVSILKVPSSKGICTAFSTCGS 243
QY 244 HLIVGMFGAATFMVYLPSSFSHPKODNIIISVFTYTPALNPLIYSLRNKVMKALRR 303
DB 244 HLSVSLFTYTVIGLYICSSANSSTLKDVTWAMMYTVVTMLNDFIYSLRNKVMKALSR 303
QY 304 VL 305
DB 304 VI 305

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RESULT 13
US-09-546-986A-8
Sequence 8, Application US/09546986A
Patent No. 6635741
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Tularik, Gene
APPLICANT: Tularik, Inc.
TITLE OF INVENTION: No. 6635741e1 G-Protein Coupled Receptors
FILE REFERENCE: 018781-004720US
CURRENT APPLICATION NUMBER: US/09/546,986A
CURRENT FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 09/524,730

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; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-985A-8

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Query Match	38.5%;	Score 616;	DB 4;	Length 334;
Best Local Similarity	40.6%;	Pred. NO. 1.1e-48;		
Matches 121; Conservative	59;	Mismatches 118;	Indels 0;	Gaps 0;

QY 10 SGIIVGLINDSSPELIVATFIILIMALTNSGLILATITAEALHPVILIGOLSIM 69
 Db 30 AGFIIIGFSDYAOQVILFVILILVILILIGNTIIIVLSRIEPLGNPMVIFELSHSEFL 89
 QY 70 DLIPTSVYTPKALADFLRENTISFEGCALQWFLATNGSADLILAFMAVDRYVAICHP 123
 Db 90 YRCFTSSVFPOLLVNLMEPMKTIAYGGCVLHVHYNHSHALGSTECVLPALMSCDRYAVACRP 144
 QY 130 LKMTLMSRVCWIMVATSMILASILAIGHWTYVHLPECVSWELRHLCIEPIPLTKAC 189
 Db 150 LHTVLMNHILHLCALLASMAVMSGIATTVQSLITLQLPFCGRQVDHITCEVPVILIKAC 209
 QY 190 ADHSRELLIIYTGVTFLILPTISAIVASTVLVFLVLMPSNEGRKALVTCSSHILVYG 245
 Db 210 VGTTEBAELFVASILFVLIVPVSFLIVSGYIAHVILIKRSATGQKAFGTCFHLTVVT 265
 QY 250 MFYCATFMVVLVSSPHSKODNISVFTIITVPLANPELITSLRKEXEMARLARBVLK 307
 Db 270 IFYGTIIIFMYLQPAKRSRSDQGRFVSLFTVTVTRNLNPELITLIRKEVKKALVVLAK 327

RESULT 14
US-09-524-730-8
; Sequence 8, Application US/09524730

Query Match	38.5%;	Score 616;	DB 4;	Length 334;
Best Local Similarity	40.6%;	Pred. No. 1.1e-48;		
Matches 121; Conservative	59;	Mismatches 118;	Indels 0;	Gaps 0

[illegible][illegible]

RESULT 15
US-09-546-986A-2
; Sequence 2, Application US/09546986A
; Date of Invention 09/27/2009

Query Match	37.8%;	Score 605;	DB 4;	Length 310;
Best Local Similarity	40.8%;	Pred. No. 1e-47;		
Matches 122;	Conservative 63;	Mismatches 108;	Indels 6;	Gaps 2

[illegible]

Search completed: August 18, 2004, 08:59:34
Job time : 20 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2004, 08:58:44 ; Search time 46 Seconds

(Without alignments)
2156.543 Million cell updates/sec

Title: US-10-024-444B-2

Perfect score: 1602

Sequence: 1 MELNSTLGSFGLVGIIND.....VNRALRVLYGKTYLAAHSTL 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1602	100.0	316	14	US-10-024-444B-2
2	1393	87.0	324	10	US-09-974-591-12
3	1393	87.0	324	10	US-09-974-591-14
4	1393	87.0	324	10	US-09-777-789-11
5	1393	87.0	324	10	US-09-974-149-12
6	1393	87.0	324	10	US-09-974-149-14
7	1390	86.8	316	9	US-09-886-055-197
8	1390	86.8	316	10	US-09-777-789-9
9	1390	86.8	316	10	US-09-804-291-197
10	1390	86.8	316	11	US-09-912-976-53
11	1390	86.8	316	11	US-09-965-422-58
12	1390	86.8	316	12	US-10-343-650A-514
13	1390	86.8	316	14	US-10-220-382-18
14	1390	86.8	316	14	US-10-017-161-310
15	1390	86.8	316	14	US-10-024-444B-3

16	1390	86.8	316	15	US-10-300-846-26	Sequence 26, Appl
17	1390	86.8	316	15	US-10-292-798-276	Sequence 276, App
18	1324	82.6	316	10	US-09-795-271-51	Sequence 51, Appl
19	1324	82.6	316	14	US-10-024-444B-4	Sequence 4, Appl
20	1312	81.9	316	11	US-09-912-976-51	Sequence 51, Appl
21	1312	81.9	316	14	US-10-024-444B-5	Sequence 5, Appl
22	1308	81.6	316	11	US-09-912-976-50	Sequence 50, Appl
23	1308	81.6	316	11	US-09-965-422-60	Sequence 60, Appl
24	1308	81.6	316	14	US-10-024-444B-6	Sequence 6, Appl
25	1304	81.4	316	10	US-09-777-789-41	Sequence 41, Appl
26	1304	81.4	316	10	US-09-777-789-42	Sequence 42, Appl
27	1304	81.4	316	10	US-09-777-789-46	Sequence 46, Appl
28	1304	81.4	316	10	US-09-777-789-47	Sequence 47, Appl
29	1304	81.4	316	10	US-09-795-271-48	Sequence 48, Appl
30	1304	81.4	316	11	US-09-912-976-52	Sequence 52, Appl
31	1304	81.4	316	11	US-09-965-422-56	Sequence 56, Appl
32	1304	81.4	316	14	US-10-024-444B-7	Sequence 7, Appl
33	1304	81.4	316	15	US-10-005-041A-104	Sequence 104, Appl
34	1248	77.9	319	10	US-09-795-271-50	Sequence 50, Appl
35	1248	77.9	319	11	US-09-965-422-57	Sequence 57, Appl
36	1203	75.1	315	10	US-09-795-271-49	Sequence 49, Appl
37	1203	75.1	315	11	US-09-965-422-59	Sequence 59, Appl
38	1203	75.1	315	11	US-09-981-566A-71	Sequence 71, Appl
39	1203	75.1	315	15	US-10-005-041A-105	Sequence 105, App
40	1083	67.6	210	14	US-10-017-161-636	Sequence 636, App
41	839	52.4	317	11	US-09-965-422-16	Sequence 16, Appl
42	833	52.0	317	9	US-09-886-055-479	Sequence 479, App
43	833	52.0	317	10	US-09-804-291-479	Sequence 14, Appl
44	833	52.0	317	11	US-09-965-422-14	Sequence 2, Appl
45	833	52.0	317	14	US-10-017-161-2	

ALIGNMENTS

RESULT 1

US-10-024-444B-2

Sequence 2, Application US/10024444B

Publication No. US20030165858A1

GENERAL INFORMATION:

APPLICANT: Padigan, Muralidhara

APPLICANT: Gerlach, Valerie L.

APPLICANT: Smithson, Glenda

APPLICANT: Stone, David

APPLICANT: Bin-Yang, Ruy

APPLICANT: Conley, Pamela B.

APPLICANT: Hart, Matthew

APPLICANT: Tomlinson, James E.

APPLICANT: Topper, James N.

APPLICANT: Kekuda, Ramesh

APPLICANT: Casman, Stacie J.

APPLICANT: MacDougall, John R.

APPLICANT: Shlomik, Edinger R.

TITLE OF INVENTION: No. US20030165858A1 GPCR-Like Proteins and Nucleic Acids Encodi

FILE REFERENCE: 21402-224 AG

CURRENT APPLICATION NUMBER: US/10/024,444B

PRIOR FILING DATE: 2002-12-19

PRIOR APPLICATION NUMBER: 60/256635

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 316

TYPE: PRT

ORGANISM: Human

US-10-024-444B-2

Query Match 100.0%; Score 1602; DB 14; Length 316;
Best Local Similarity 100.0%; Pred. No. 1,5e-144;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELNSTLGSFGLVGIINDSGSPPELLVATFTIYMLATLTSNGILLATITRARIHPMY 60

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Db      1 MELRNSTLSSGFLVGLINDSGSPDLVATFTLLMALTNSGLLALTTEARLHMPY 60
Qy      61 LILGQLSMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTWGSADLLAFMAY 120
Db      61 LILGQLSMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTWGSADLLAFMAY 120
Qy      121 DRYVAICHPLKWTMTSPRCWTMTVATSWTILASLAIIGHMTYMHLPFCVSWETRHLCE 180
Db      121 DRYVAICHPLKWTMTSPRCWTMTVATSWTILASLAIIGHMTYMHLPFCVSWETRHLCE 180
Qy      181 IPELKLACADTSRYELIIVYGVTELLPISAIVASYTLVLTFTVLRMPSEGRKKALVT 240
Db      181 IPELKLACADTSRYELIIVYGVTELLPISAIVASYTLVLTFTVLRMPSEGRKKALVT 240
Qy      241 CSNHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
Db      241 CSNHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
Qy      301 LRRVLGKYLIAHSTL 316
Db      301 LRRVLGKYLIAHSTL 316
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RESULT 2

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US-09-974-591-12
; Sequence 12, Application US/09974591
; Publication No. US20030059830A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Murajidhara
; APPLICANT: Spytek, Kimberly A
; TITLE OF INVENTION: No. US20030059830A1 Single Nucleotide Polymorphisms for Olfaction
; TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding
; FILE REFERENCE: 15966-654 CIP
; CURRENT APPLICATION NUMBER: US/09/974,591
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/245,292
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-591-12
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Query Match      87.0%; Score 1393; DB 10; Length 324;
Best Local Similarity 87.3%; Pred. No. 1.4e-124;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;
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Db      9 MELRNFTLSSGFLVGLINDSGSPDLVATFTLLMALTNSGLLALTTEARLHMPY 68
Qy      61 LILGQLSMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTWGSADLLAFMAY 120
Db      69 LILGQLSMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTWGSADLLAFMAY 128
Qy      121 DRYVAICHPLKWTMTSPRCWTMTVATSWTILASLAIIGHMTYMHLPFCVSWETRHLCE 180
Db      129 DRYVAICHPLKWTMTSPRCWTMTVATSWTILASLAIIGHMTYMHLPFCVSWETRHLCE 188
Qy      181 IPELKLACADTSRYELIIVYGVTELLPISAIVASYTLVLTFTVLRMPSEGRKKALVT 240
Db      189 IPELKLACADTSRYELIIVYGVTELLPISAIVASYTLVLTFTVLRMPSEGRKKALVT 248
Qy      241 CSNHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
Db      241 CSNHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
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Db      249 CSNHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 308
Qy      301 LRRVLGKYLIAHSTL 316
Db      309 LRRVLGKYLIAHSTL 324
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RESULT 3

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US-09-974-591-14
; Sequence 14, Application US/09974591
; Publication No. US20030059830A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Burgess, Catherine E
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Padigaru, Murajidhara
; APPLICANT: Spytek, Kimberly A
; TITLE OF INVENTION: No. US20030059830A1 Single Nucleotide Polymorphisms for Olfaction
; TITLE OF INVENTION: Receptor-like Polypeptides and Nucleic Acids Encoding
; FILE REFERENCE: 15966-654 CIP
; CURRENT APPLICATION NUMBER: US/09/974,591
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/245,292
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-591-14
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Query Match      87.0%; Score 1393; DB 10; Length 324;
Best Local Similarity 87.3%; Pred. No. 1.4e-124;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;
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Qy      1 MELRNSTLSSGFLVGLINDSGSPDLVATFTLLMALTNSGLLALTTEARLHMPY 60
Db      9 MELRNFTLSSGFLVGLINDSGSPDLVATFTLLMALTNSGLLALTTEARLHMPY 68
Qy      61 LILGQLSMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTWGSADLLAFMAY 120
Db      69 LILGQLSMDLFTSVTPKALADFLRRENTISFGGCAIQMFALTWGSADLLAFMAY 128
Qy      121 DRYVAICHPLKWTMTSPRCWTMTVATSWTILASLAIIGHMTYMHLPFCVSWETRHLCE 180
Db      129 DRYVAICHPLKWTMTSPRCWTMTVATSWTILASLAIIGHMTYMHLPFCVSWETRHLCE 188
Qy      181 IPELKLACADTSRYELIIVYGVTELLPISAIVASYTLVLTFTVLRMPSEGRKKALVT 240
Db      189 IPELKLACADTSRYELIIVYGVTELLPISAIVASYTLVLTFTVLRMPSEGRKKALVT 248
Qy      241 CSNHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 300
Db      249 CSNHLIVGMFYGAATFMYVLPSSFSHPKODNIISVFTYITVPALNPLIYSLRNKEVMA 308
Qy      301 LRRVLGKYLIAHSTL 316
Db      309 LRRVLGKYLIAHSTL 324
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RESULT 4

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US-09-777-789-11
; Sequence 11, Application US/09777789
; Publication No. US20030087815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-654
; CURRENT APPLICATION NUMBER: US/09/777,789
; CURRENT FILING DATE: 2001-05-11
```

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/ PRIOR APPLICATION NUMBER: 60/180,646
/ PRIOR FILING DATE: 2000-02-07
/ NUMBER OF SEQ ID NOS: 101
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 324
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-777-789-11

Query Match
Best Local Similarity 87.0%; Score 1393; DB 10; Length 324;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTGSGFLVGIINDSGSPPELLVATFTILYMLALTSNGLLAITTEARLHMPY 60
DB 9 MELMNFLLGSGFLVGIINDSGSPPELLCAITITLYLALISNGLLAITTEARLHMPY 68
QY 61 LLLGQLSMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 120
DB 69 LLLGQLSMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 128
QY 121 DRYVAICHPDKMTIMSPRCWIMVATSWILASLAIGHMTYTMHLPCVSWERHLLCE 180
DB 129 DRYVAICHPDKMTIMSPRCWIMVATSWILASLAIGHMTYTMHLPCVSWERHLLCE 188
QY 181 IPEPLKACADTSRELIYYTGVTFLIPISAIYASVTLVFTVLRMPSNCKKALVT 240
DB 189 IPHLKACADTSRELIYYTGVTFLIPISAIYASVTLVFTVLRMPSNCKKALVT 248
QY 241 CSSHLIVGMFGAATFMYLPSFSFSPKODNISVEFTITVPALNPLIYSLRNKEWMA 300
DB 249 CSSHLIVGMFGAATFMYLPSFSFSPKODNISVEFTITVPALNPLIYSLRNKEWMA 308
QY 301 LRRVLGKYTLIAHSTL 316
DB 309 LRRVLGKYTLIAHSTL 324

RESULT 5
US-09-974-149-12
/ Sequence 12, Application US/09974149
/ Publication No. US20030175705A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Grose, William M
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Bader, Joel S
/ TITLE OF INVENTION: Methods of Use for No. US20030175705A1 Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
/ FILE REFERENCE: 15966-654UB
/ CURRENT APPLICATION NUMBER: US/09/974,149
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: 60/323,755
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 324
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-974-149-12

Query Match
Best Local Similarity 87.0%; Score 1393; DB 10; Length 324;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTGSGFLVGIINDSGSPPELLVATFTILYMLALTSNGLLAITTEARLHMPY 60
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DB 9 MELMNFLLGSGFLVGIINDSGSPPELLCAITITLYLALISNGLLAITTEARLHMPY 68
QY 61 LLLGQLSMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 120
DB 69 LLLGQLSMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 128
QY 121 DRYVAICHPDKMTIMSPRCWIMVATSWILASLAIGHMTYTMHLPCVSWERHLLCE 180
DB 129 DRYVAICHPDKMTIMSPRCWIMVATSWILASLAIGHMTYTMHLPCVSWERHLLCE 188
QY 181 IPEPLKACADTSRELIYYTGVTFLIPISAIYASVTLVFTVLRMPSNCKKALVT 240
DB 189 IPHLKACADTSRELIYYTGVTFLIPISAIYASVTLVFTVLRMPSNCKKALVT 248
QY 241 CSSHLIVGMFGAATFMYLPSFSFSPKODNISVEFTITVPALNPLIYSLRNKEWMA 300
DB 249 CSSHLIVGMFGAATFMYLPSFSFSPKODNISVEFTITVPALNPLIYSLRNKEWMA 308
QY 301 LRRVLGKYTLIAHSTL 316
DB 309 LRRVLGKYTLIAHSTL 324

RESULT 6
US-09-974-149-14
/ Sequence 14, Application US/09974149
/ Publication No. US20030175705A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Grose, William M
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Bader, Joel S
/ TITLE OF INVENTION: Methods of Use for No. US20030175705A1 Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms of Olfactory Receptor-like Polypeptides
/ FILE REFERENCE: 15966-654UB
/ CURRENT APPLICATION NUMBER: US/09/974,149
/ PRIOR FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: 60/323,755
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 324
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-974-149-14

Query Match
Best Local Similarity 87.0%; Score 1393; DB 10; Length 324;
Matches 276; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTGSGFLVGIINDSGSPPELLVATFTILYMLALTSNGLLAITTEARLHMPY 60
DB 9 MELMNFLLGSGFLVGIINDSGSPPELLCAITITLYLALISNGLLAITTEARLHMPY 68
QY 61 LLLGQLSMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 120
DB 69 LLLGQLSMDLLFTSVTPKALADFLRRENTISFGGCAQMPALTMGSAEDLLAFMAY 128
QY 121 DRYVAICHPDKMTIMSPRCWIMVATSWILASLAIGHMTYTMHLPCVSWERHLLCE 180
DB 129 DRYVAICHPDKMTIMSPRCWIMVATSWILASLAIGHMTYTMHLPCVSWERHLLCE 188
QY 181 IPEPLKACADTSRELIYYTGVTFLIPISAIYASVTLVFTVLRMPSNCKKALVT 240
DB 189 IPHLKACADTSRELIYYTGVTFLIPISAIYASVTLVFTVLRMPSNCKKALVT 248
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QY 241 CSSHLIVGMFGAATPMYVLPSSFSHPKODNIISVFYITVTPALNPILYSLRNKEVWRA 300
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 249 CSSHLIVGMFGAATPMYVLPSSFSHPKODNIISVFYITVTPALNPILYSLRNKEVWRA 308
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 301 LRRVLGKYTLIAHSTL 316
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 309 LRRVLGKYMLPAHSTL 324
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 7
US-09-886-055-197
; Sequence 197, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886, 055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213, 812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 197
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-197

Query Match 86.8%; Score 1390; DB 9; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0

QY 1 MELNSTLGSFLLVGLINDSGSPPELLYATFTILYMLALTSNGLLLAITTEARLHMPY 60
Db 1 MELNFTLGSGFLLVGLINDSGSPPELLCATITILYMLAISGGLLAIITMARLHMPY 60
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 61 LLLGQLSMDLLFTSVTPKALADFLRRENTISFGGCAQLMFALITMGSABDLIAFMAY 120
Db 61 LLLGQLSMDLLFTSVTPKALADFLRRENTISFGGCAQLMFALITMGSABDLIAFMAY 120
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 121 DRYAACHPLKMTLMSPRVCIMATSWIIASLAIAGHTWMTMLPCVSMIRHILCE 180
Db 121 DRYAACHPLTYMTLMSSPACWLMAWTSWIIASLSALITYVTMHPFCRAQRIHILCE 180
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 181 IPELKLACADPTSRYELIIVYGVTFLLPISAIYASYLVLFVLRMPNSNGRKKALVT 240
Db 181 IPELKLACADPTSRKELMAYVGVTFLLPISLAIIASYQILLIYLRMPNSNGRKKALVT 240
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 241 CSSHLIVGMFGAATPMYVLPSSFSHPKODNIISVFYITVTPALNPILYSLRNKEVWRA 300
Db 241 CSSHLIVGMFGAATPMYVLPSSFSHPKODNIISVFYITVTPALNPILYSLRNKEVWRA 300
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 301 LRRVLGKYTLIAHSTL 316
Db 301 LRRVLGKYMLPAHSTL 316
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 8
US-09-777-789-9
; Sequence 9, Application US/09777789
; Publication No. US20030087815A1
; GENERAL INFORMATION:
; APPLICANT: Padigar et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15366-654
; CURRENT APPLICATION NUMBER: US/09/777, 789
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/180, 646
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 101

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 316
; TYPE: PR1
; ORGANISM: Homo sapiens
US-03-777-789-9

Query Match      86.8%; Score 1390; DB 10; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0

Db      1 MELNSTGSGFFIIIVGILNDGSGPELIIATFTIILYMLALITSGNGLIIIIATITIEARLHPMY 60
1 MELNFTIGSGFFIIIVGILNDGSGPELIIATITIIYILIALISNGLIILIIATTEARLHPMY 60

QY      1 LILIGQLSMDLIFTSVTPPKALADLRRENTISFGGALQMLALTMGAEDLLAFMY 120
61 LILIGQLSMDLIFTSVTPPKALADLRRENTISFGGALQMLALTMGAEDLLAFMY 120
DB      61 LILIGQLSMDLIFTSVTPPKALADLRRENTISFGGALQMLALTMGAEDLLAFMY 120
61 LILIGQLSMDLIFTSVTPPKALADLRRENTISFGGALQMLALTMGAEDLLAFMY 120

QY      121 DRYVAICHPLKYMTLMSPRVCMIVATSWIIASLIAIGHYTYMHLPCVSWERHLICE 180
121 DRYVAICHPLKYMTLMSPRVCMIVATSWIIASLIAIGHYTYMHLPCVSWERHLICE 180
DB      121 DRYVAICHPLKYMTLMSPRVCMIVATSWIIASLIAIGHYTYMHLPCVSWERHLICE 180
121 DRYVAICHPLKYMTLMSPRVCMIVATSWIIASLIAIGHYTYMHLPCVSWERHLICE 180

QY      181 IPELIIKACAPTSRVELIIYVGTGTELLPIISAIYASYTLVLPFYLRMPNSNEGRKALYT 240
181 IPELIIKACAPTSRVELIIYVGTGTELLPIISAIYASYTLVLPFYLRMPNSNEGRKALYT 240
DB      181 IPELIIKACAPTSRVELIIYVGTGTELLPIISAIYASYTLVLPFYLRMPNSNEGRKALYT 240
181 IPELIIKACAPTSRVELIIYVGTGTELLPIISAIYASYTLVLPFYLRMPNSNEGRKALYT 240

QY      241 CSHSLIIVGMEYGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRNKEVMA 300
241 CSHSLIIVGMEYGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRNKEVMA 300
DB      241 CSHSLIIVGMEYGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRNKEVMA 300
241 CSHSLIIVGMEYGAATFMYVLPSSFSHPKODNIISVFYITVPALNPLIYSLRNKEVMA 300

QY      301 LRRVYGYKYLIIAHSTL 316
301 LRRVYGYKYLIIAHSTL 316
DB      301 LRRVYGYKYLIIAHSTL 316
301 LRRVYGYKYLIIAHSTL 316

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RESULT 9
US-09-804-291-197
; Sequence 197, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 02/8005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 197
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291-197
Query Match      86.8%; Score 1390; DB 10; Length 316;

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Best Local Similarity 87.0%; Pred. No. 2,66-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLLVGLINDSGSPPELLVATFTLLVMTALTSNGLLIATITTEARLHMPY 60
DB 1 MELMNTLSSGFLVGLINDSGSPPELLCATITTLVILALISNGLLIATITTEARLHMPY 60
QY 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAQMFALTMGAEEDLLAFMAY 120
DB 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAQMFALTMGAEEDLLAFMAY 120
QY 121 DRYVAICHPLTMTLMSRPAWMTATSWILASLALIGHMTYTMHLPFCVSMERILHCE 180
DB 121 DRYVAICHPLTMTLMSRPAWMTATSWILASLALIGHMTYTMHLPFCVSMERILHCE 180
QY 181 IPELKLACADTSRYELIIVYTVTEFLIPISAIIVASYTLVFTVLRMPSNEGRKKALVT 240
DB 181 IPELKLACADTSRYELIIVYTVTEFLIPISAIIVASYTLVFTVLRMPSNEGRKKALVT 240
QY 241 CSNHLIVGMFGAATFMVLPSSPFSHPKODNIISVFYITVTPALNPLIYSLRKEVMA 300
DB 241 CSNHLIVGMFGAATFMVLPSSPFSHPKODNIISVFYITVTPALNPLIYSLRKEVMA 300
QY 301 LRRVIGKYLILAHSTL 316
DB 301 LRRVIGKYLILAHSTL 316

RESULT 10

US-09-912-976-53
Sequence 53, Application US/09912976
Publication No. US20030212255A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mezes, Peter
APPLICANT: Burgess, Catherine
APPLICANT: Casman, Stacie
APPLICANT: Grose, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-070
CURRENT APPLICATION NUMBER: US/09/912,976
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/221,336
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/238,333
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/260,675
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/271,025
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/278,164
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/280,876
PRIOR FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 53
LENGTH: 316
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-976-53

Query Match 86.8%; Score 1390; DB 11; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,66-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELRNSTLGGFLLVGLINDSGSPPELLVATFTLLVMTALTSNGLLIATITTEARLHMPY 60

DB 1 MELMNTLSSGFLVGLINDSGSPPELLCATITTLVILALISNGLLIATITTEARLHMPY 60
QY 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAQMFALTMGAEEDLLAFMAY 120
DB 61 LILGQSLMDLFTSVTPKALADFLRRENTISFGGCAQMFALTMGAEEDLLAFMAY 120
QY 121 DRYVAICHPLTMTLMSRPAWMTATSWILASLALIGHMTYTMHLPFCVSMERILHCE 180
DB 121 DRYVAICHPLTMTLMSRPAWMTATSWILASLALIGHMTYTMHLPFCVSMERILHCE 180
QY 181 IPELKLACADTSRYELIIVYTVTEFLIPISAIIVASYTLVFTVLRMPSNEGRKKALVT 240
DB 181 IPELKLACADTSRYELIIVYTVTEFLIPISAIIVASYTLVFTVLRMPSNEGRKKALVT 240
QY 241 CSNHLIVGMFGAATFMVLPSSPFSHPKODNIISVFYITVTPALNPLIYSLRKEVMA 300
DB 241 CSNHLIVGMFGAATFMVLPSSPFSHPKODNIISVFYITVTPALNPLIYSLRKEVMA 300
QY 301 LRRVIGKYLILAHSTL 316
DB 301 LRRVIGKYLILAHSTL 316

RESULT 11

US-09-965-422-58
Sequence 58, Application US/09965422
Publication No. US20030216545A1
GENERAL INFORMATION:
APPLICANT: Spylek, Kimberly A
APPLICANT: Casman, Stacie
APPLICANT: Padigaru, Muralidhara
APPLICANT: Dickson, Kevin
APPLICANT: Vernet, Corine
APPLICANT: Spaderna, Steven K
APPLICANT: Shenoy, Suresh G
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: Edinger, Shlomit
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glenda
APPLICANT: Li, Li
APPLICANT: Malpankar, Urial M
APPLICANT: Taylor, Sarah
APPLICANT: Gunther, Erik
APPLICANT: Tchernyev, Velizar T
TITLE OF INVENTION: No. US0030216545A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21401-132
CURRENT APPLICATION NUMBER: US/09/965,422
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,286
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/236,284
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/237,581
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238,735
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/240,736
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/260,019
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,338
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/262,156
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/262,498
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/263,133
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,691
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/266,109

;; PRIOR FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: 60/271,634
;; PRIOR FILING DATE: 2001-02-26
;; NUMBER OF SEQ ID NOS: 127
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 58
;; LENGTH: 316
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-965-422-58

Query Match 86.8%; Score 1390; DB 11; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIIVGILNDSGPELLYATFTIYMLATNSGILLATITTEARLHMPY 60
DB 1 MELNFTLGSGLIIVGILNDSGPELLCATITTIYLLALISNGILLATITTEARLHMPY 60
QY 61 LLLGQLSIMDLFTSVTPPKALADFLRENTISFGGALQMFALTWGABDILLAFMAY 120
DB 61 LLLGQLSIMDLFTSVTPPKALADFLRENTISFGGALQMFALTWGABDILLAFMAY 120
QY 121 DRYVAICHPLKMTLMSRVCWIMVATSWILASILAIGHMTYMLPFCVSWETRHLICE 180
DB 121 DRYVAICHPLKMTLMSRVCWIMVATSWILASILAIGHMTYMLPFCVSWETRHLICE 180
QY 181 IPRLLKACADTSRYELIYVGTFTLLPISAVASYTLVFTVLRMPSNEGRKKALVT 240
DB 181 IPRLLKACADTSRYELIYVGTFTLLPISAVASYTLVFTVLRMPSNEGRKKALVT 240
QY 241 CSSHLIVGMFYGAATFMYVLPSSFHSPKQDNISVFYITVPALNPLIYSLRKEVWRA 300
DB 241 CSSHLIVGMFYGAATFMYVLPSSFHSPKQDNISVFYITVPALNPLIYSLRKEVWRA 300
QY 301 LRRVLGYILLAHSTL 316
DB 301 LRRVLGYILLAHSTL 316

RESULT 12
US-10-343-650A-514
;; Sequence 514, Application US/10343650A
;; Publication No. US20040067499A1
;; GENERAL INFORMATION:
;; APPLICANT: HAGA, TATSUYA
;; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
;; FILE REFERENCE: 31671-186347
;; CURRENT APPLICATION NUMBER: US/10/343,650A
;; CURRENT FILING DATE: 2003-07-21
;; PRIOR APPLICATION NUMBER: JP 2000/237818
;; PRIOR FILING DATE: 2000-08-04
;; PRIOR APPLICATION NUMBER: JP 2001/34434
;; PRIOR FILING DATE: 2001-02-13
;; NUMBER OF SEQ ID NOS: 694
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 514
;; LENGTH: 316
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-343-650A-514

Query Match 86.8%; Score 1390; DB 12; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIIVGILNDSGPELLYATFTIYMLATNSGILLATITTEARLHMPY 60
DB 1 MELNFTLGSGLIIVGILNDSGPELLCATITTIYLLALISNGILLATITTEARLHMPY 60
QY 61 LLLGQLSIMDLFTSVTPPKALADFLRENTISFGGALQMFALTWGABDILLAFMAY 120
DB 61 LLLGQLSIMDLFTSVTPPKALADFLRENTISFGGALQMFALTWGABDILLAFMAY 120

QY 121 DRYVAICHPLKMTLMSRVCWIMVATSWILASILAIGHMTYMLPFCVSWETRHLICE 180
DB 121 DRYVAICHPLKMTLMSRVCWIMVATSWILASILAIGHMTYMLPFCVSWETRHLICE 180
QY 181 IPRLLKACADTSRYELIYVGTFTLLPISAVASYTLVFTVLRMPSNEGRKKALVT 240
DB 181 IPRLLKACADTSRYELIYVGTFTLLPISAVASYTLVFTVLRMPSNEGRKKALVT 240
QY 241 CSSHLIVGMFYGAATFMYVLPSSFHSPKQDNISVFYITVPALNPLIYSLRKEVWRA 300
DB 241 CSSHLIVGMFYGAATFMYVLPSSFHSPKQDNISVFYITVPALNPLIYSLRKEVWRA 300
QY 301 LRRVLGYILLAHSTL 316
DB 301 LRRVLGYILLAHSTL 316

RESULT 13
US-10-220-382-18
;; Sequence 18, Application US/10220382
;; Publication No. US2003011911A1
;; GENERAL INFORMATION:
;; APPLICANT: INCYTE GENOMICS, INC.
;; APPLICANT: LAL, Preeti
;; APPLICANT: TANG, Y. Tom
;; APPLICANT: PATERSON, Chandra
;; APPLICANT: YAO, Monique G.
;; APPLICANT: SHIH, Leo L.
;; APPLICANT: TRIBOULEY, Catherine
;; APPLICANT: LU, Dzung Anna M.
;; APPLICANT: YUE, Henry
;; APPLICANT: KHAN, Farrah A.
;; APPLICANT: POLICKY, Jennifer L.
;; APPLICANT: AU-YOUNG, Janice
;; APPLICANT: YANG, Junming
;; APPLICANT: HARLAND, Lee
;; APPLICANT: WALSH, Roderick T.
;; APPLICANT: LO, Terence P.
;; APPLICANT: BOROMSKY, Mark L.
;; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;; FILE REFERENCE: PI-0044 PCT
;; CURRENT APPLICATION NUMBER: US/10/220,382
;; CURRENT FILING DATE: 2001-03-01
;; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
;; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PERL Program
;; SEQ ID NO 18
;; LENGTH: 316
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: incyte ID No. US2003011911A1 7472446CD1
US-10-220-382-18

Query Match 86.8%; Score 1390; DB 14; Length 316;
Best Local Similarity 87.0%; Pred. No. 2,6e-124;
Matches 275; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

QY 1 MELNSTLGSGLIIVGILNDSGPELLYATFTIYMLATNSGILLATITTEARLHMPY 60
DB 1 MELNFTLGSGLIIVGILNDSGPELLCATITTIYLLALISNGILLATITTEARLHMPY 60
QY 61 LLLGQLSIMDLFTSVTPPKALADFLRENTISFGGALQMFALTWGABDILLAFMAY 120
DB 61 LLLGQLSIMDLFTSVTPPKALADFLRENTISFGGALQMFALTWGABDILLAFMAY 120
QY 121 DRYVAICHPLKMTLMSRVCWIMVATSWILASILAIGHMTYMLPFCVSWETRHLICE 180
DB 121 DRYVAICHPLKMTLMSRVCWIMVATSWILASILAIGHMTYMLPFCVSWETRHLICE 180

Qy	181	IPPLIKLACDTSRRELIIYVGVFLLPISAIVASYTLVFTVLRMPNSGRKKALVT	240
Db	181	IPHLIKVACDTSRRELIMVYMGVTFLLPSLAIILASTYQIILLTVLRMPNSGRKKALVT	240
Qy	241	CSHLLIVGMFYGAATFMVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRNKEVMA	300
Db	241	CSHLLTVGMFYGAATFMVLPSSFSHSTRQDNIIISVFYITVTPALNPLIYSLRNKEVMA	300
Qy	301	LRRVLGKTYLLAHSTL 316	
Db	301	LRRVLGKTYMLPAHSTL 316	
RESULT 14			
US-10-017-161-310			
/ Sequence 310, Application US/10017161			
/ Publication No. US20030143668A1			
/ GENERAL INFORMATION:			
/ APPLICANT: SUMA, MAKIKO			
/ APPLICANT: ASAI, KIYOSHI			
/ APPLICANT: AKIYAMA, YUTAKA			
/ APPLICANT: ABURATANI, HIROYUKI			
/ TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS			
/ FILE REFERENCE: 08435/0152			
/ CURRENT APPLICATION NUMBER: US/10/017, 161			
/ CURRENT FILING DATE: 2002-12-18			
/ PRIOR APPLICATION NUMBER: JP 2001/246789			
/ PRIOR FILING DATE: 2001-06-18			
/ NUMBER OF SEQ ID NOS: 2430			
/ SOFTWARE: PatentIn Ver. 2.1			
/ SEQ ID NO 310			
/ LENGTH: 316			
/ TYPE: PRT			
/ ORGANISM: Homo sapiens			
US-10-017-161-310			
Query Match	86.8%	Score 1390;	DB 14; Length 316;
Best Local Similarity	87.0%;	Pred. No. 2.6e-124;	
Matches 275;	Conservative 17;	Mismatches 24;	Indels 0; Gaps 0
Qy	1	MELNSTLGSGLVIGLINDSGSPPELLVATFTILVMALTSNGLLATITTEARLMPY	60
Db	1	MELNFTLGSGLVIGLINDSGSPPELLCTITITLIVLALISNGLLATITTEARLMPY	60
Qy	61	LLLGQLSLMDLLFTSVTPPKALADFLRRENTISFPGCALQMFALTMGSAEDLLAFMAY	120
Db	61	LLLGQLSLMDLLFTSVTPPKALADFLRRENTISFPGCALQMFALTMGSAEDLLAFMAY	120
Qy	121	DRYVALCHPLKMTMTSPRVCKIMATSWITASLAIIGHMTYTMELPFCVSWEIRLLCE	180
Db	121	DRYVALCHPLTYMTMTSSRACMLWATSWITASLAIYVYTMHYPFRAOEIRHLLCE	180
Qy	181	IPPLIKLACDTSRRELIIYVGVFLLPISAIVASYTLVFTVLRMPNSGRKKALVT	240
Db	181	IPHLIKVACDTSRRELIMVYMGVTFLLPSLAIILASTYQIILLTVLRMPNSGRKKALVT	240
Qy	241	CSHLLIVGMFYGAATFMVLPSSFSHPKODNIIISVFYITVTPALNPLIYSLRNKEVMA	300
Db	241	CSHLLTVGMFYGAATFMVLPSSFSHSTRQDNIIISVFYITVTPALNPLIYSLRNKEVMA	300
Qy	301	LRRVLGKTYLLAHSTL 316	
Db	301	LRRVLGKTYMLPAHSTL 316	
RESULT 15			
US-10-024-444B-3			
/ Sequence 3, Application US/1002444B			
/ Publication No. US20030165858A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Padigaru, Muralidhara			
/ APPLICANT: Gerlach, Valerie L.			
/ APPLICANT: Smithson, Glennda			

```

? APPLICANT: Stone, David
? APPLICANT: Bin-Yang, Ruey
? APPLICANT: Conley, Pamela B.
? APPLICANT: Hart, Matthew
? APPLICANT: Tomlinson, James E.
? APPLICANT: Topper, James N.
? APPLICANT: Kekuda, Ramesh
? APPLICANT: Casman, Stacie J.
? APPLICANT: Macdonagall, John R.
? APPLICANT: Shlomit, Edinger R.
? TITLE OF INVENTION: No. US20030165858A1e1 GPCR-Like Proteins and Nucleic Acids Encoda
? TITLE OF INVENTION: Same
? FILE REFERENCE: 21402-224 AG
? CURRENT APPLICATION NUMBER: US/10/024,444B
? CURRENT FILING DATE: 2002-12-19
? PRIOR APPLICATION NUMBER: 60/256635
? PRIOR FILING DATE: 2000-12-18
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 3
? LENGTH: 316
? TYPE: PRT
? ORGANISM: human
US-10-024-444B-3

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Query Match	86.8%;	Score 1390;	DB 14;	Length 316;
Best Local Similarity	87.0%;	Pred. No. 2.6e-124;		
Matches 275;	Conservative 17;	Mismatches 24;	Indels 0;	Gaps 0;

[illegible]

Search completed: August 18, 2004, 09:06:28
Job time : 47 secs

RESULT 15
US-10-024-444B-3
; Sequence 3, Application US/10024444B
; Publication No. US20030165858A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Smithson, Glenda

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